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OM nucleic - nucleic search, using sw model

Run on: January 17, 2002, 23:52:22 ; Search time 1381.58 Seconds

(without alignments)
9910.869 Million cell updates/sec

Title: US-09-358-321C-31

Perfect score: 830
Sequence: 1 ctgaatggtgaagcgctat.....ctgaatggtgaagcgcgcg 830

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vl:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.om:*
20: em.or:*
21: em.ov:*
22: em.pat:*
23: em.ph:*
24: em.pl:*
25: em.ro:*
26: em.sts:*
27: em.sy:*
28: em.un:*
29: em.vl:*
30: em.hgo.hum:*
31: em.hgo.in:*
32: em.hgo.fod:*
33: em.htg.hum:*
34: em.htg.in:*
35: em.htg.rod:*
36: em.htg.other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	502.4	60.5	759	12	SCO250763	AJ250763 Mus muscu
2	501.2	60.4	1637	6	AX006750	AX006750 Sequence
3	499	60.1	753	6	AX003768	AX003768 Sequence
4	499	60.1	753	6	AX003776	AX003776 Sequence
5	482.6	58.1	864	12	XX031739	U31739 Single chai
6	476.6	57.4	732	12	XX044796	U44796 Synthetic c
7	476	57.3	792	12	AF276797	AF276797 Synthetic
8	411.6	49.6	768	6	AS7272	AS7272 Sequence 4
9	407.6	49.1	749	6	AS9386	AS9386 Sequence 36
10	403.2	48.8	1511	6	AS9381	AS9381 Sequence 31
11	404.6	48.7	729	12	AC013152	AU131532 Synthetic
12	397.2	47.9	1101	6	AB2599	AB2599 Sequence 1
13	397.2	47.9	1103	6	AB2600	AB2600 Sequence 2
14	392.8	47.3	795	10	KMSCV25	270662 Artificial
15	389.6	46.9	738	10	AF141321	AF141321 Mus muscu
16	381.6	46.0	925	6	E30617	E30617 Antibody an
17	380.4	45.8	772	6	AR085460	AR085460 Sequence
18	380.4	45.8	772	6	AR088866	AR088866 Sequence
19	380.4	45.8	772	6	136723	136723 Sequence 33
20	380.4	45.8	772	12	S57990	S57990 B3(PV)-PE40
21	380.4	45.8	912	12	AB030249	AB030249 Synthetic
22	370	44.6	747	6	A33046	A33046 Anti-oxazol
23	369.4	44.5	720	12	AF059737	AF059737 Synthetic
24	368.8	44.4	918	6	E31219	E31219 Device for
25	368.8	44.4	804	6	A95255	A95255 Sequence 1
26	367.8	44.3	747	6	AX100176	AX100176 Expression
27	367.2	44.2	879	6	E16309	E16309 DNA encodin
28	365	44.0	774	12	SCD65537	SCD65537 Synthetic M
29	364.6	43.9	825	12	SCD65536	SCD65536 Synthetic M
30	364.2	43.9	726	6	AX146641	AX146641 Sequence
31	362.4	43.7	864	6	AB3227	AB3227 Sequence 47
32	355.8	42.9	810	10	NM062527	U62527 Mus musculu
33	354.2	42.7	3970	12	ASV14585	Y14585 Artificial
34	352.6	42.5	4363	12	SCFV18290	Y18290 Expression
35	352.6	42.5	4864	12	ASV14584	Y14584 Artificial
36	352.4	42.5	747	10	NM0480	Y29480 M.musculus
37	350.2	42.2	3991	12	ASV12778	Y12778 Artificial
38	348.2	42.0	738	6	AR085459	AR085459 Sequence
39	348.2	42.0	738	6	AR088865	AR088865 Sequence
40	348.2	42.0	738	6	136722	136722 Sequence 31
41	347.4	41.9	1653	6	AX011208	AX011208 Sequence
42	347.4	41.9	1698	6	AX011206	AX011206 Sequence
43	347.4	41.9	2010	6	AR112914	AR112914 Sequence
44	344	41.4	4354	12	ASV14583	Y14583 Artificial
45	343.6	41.4	744	12	AF402256	AF402256 Synthetic

ALIGNMENTS

RESULT	1	LOCUS	SCO250763	DEFINITION	Mus musculus synthetic construct for anti-guinea pig C5 scfv	SYN	11-MAY-2000
ACCESSION	AJ250763	VERSION	AJ250763.1	KEYWORDS	GI:6272278	antibody; heavy chain; immunoglobulin superfamily; light chain; scfv; variable region.	
SOURCE	ORGANISM	REFERENCE	1 (bases 1 to 759)	AUTHORS	Link,C., Hawlicsch,H., Meyer zu Vilsendorf,A., Gylteruez,S., Nagel,E. and Koehn,U.	Selection of phage-displayed anti-guinea pig C5 or C3a antibodies and their application in xenotransplantation	
JOURNAL	REFERENCE	2 (bases 1 to 759)	AUTHORS	Link,C.			

Db	1	GAGTGCAGCGTCTCCAGCGAGTGTGAGACTGGAAGCTGGCCAGGCGCTGGGCTTCATGTGAG	60
OY	124	ctgtccctcgcaagggtctcggggtctacaattactgactatgatatacaactcgggttgaggag	183
Db	61	CTGTCTCGCAAGGCTTGTGCGTACACCTTACAAACTATGTGTTAAGCTGGGTGAAGAG	120
OY	184	aacacttgatggccctggaatgatgttgaggcattgatccctggaactggtgtatctgc	243
Db	121	AGGCTTGACAGGGTCTTGATGTGATTTGGAGAGGTTTATCTGAGATTGGTATCTTAC	180
OY	244	tacaataagaagtttcaaggacaaggccatagtgtaactgtaagacaataccctccagacagcc	303
Db	181	TACAAATGAGAAGTTCAAGGGCCAAAGGCCACACTGCTGCAGACAAATTCCTCCAGCAGACG	240
OY	304	tacattgaagctccgcaagccctggaattctgaagactctgcgcgtctattactatacaaatg	363
Db	241	TTCATGAGAGCTCCGACACCTTGACCTTGAGAGACTGCGCGTATTCTGTGCAAGAGCG	300
OY	364	-----ttggaagacttggggccaagagactctgtc	393
Db	301	GGATCTCAACGATFACATCTACAGACTGCTGACTTGTGATGTCTGGGGCCAAAGGACACGGT	360
OY	384	actgtctctgca---gagggtaaactcctcaagatctgtgctccgaaatccaaacccgggag	450
Db	361	ACCGTCTCTCAGGTGTGTGTGTGTGTGTGGCGGCGCGCTCCGGTGTGTGTGTGTGAG	420
OY	451	gtgtgtgtgaccccaaaccaacacacctccgcgtccgtgaactcgtggaatgaacccacac	510
Db	421	CTCGTGATGACCCGAGACTCCACTCTCCCTGCTGTGTAGTCTTGGAGATTAACCTTCATC	480
OY	511	tcttgcagatctagtcagagccctttacaagtaatgatgaatcaactatttactgtgtac	570
Db	481	TCTTGCAAGATCTATCTAGACACCTTTGACAGTAAGTAAGAAACACCTATTACATGTGAC	540
OY	571	cttgaagaagccagggccgctcttccaaagctctcgtatatacaagtttccaacgatttct	630
Db	541	CTGCAAGAGCCAGGCCAGCTCTCCAAAGCTCTGTATCTACAAAGTTTCCAACCGATTTC	600
OY	631	gggggtcccaagacaggttcacgttgacgtgacgtgacgtgacgtgacgtgacgtgacgt	690
Db	601	GGGGTCCAGACAGATTCACTGTGACGTGACGTGACGTGACGTGACGTGACGTGACGTGAC	660
OY	651	agaatgagagcttgaggatctcgggaattattctctgtcccaagtaacacatgttccgtac	750
Db	661	AGAATGAGAGGCTGAGGATCTGGGAGATTATTTCTGCTCTCAAGATACATATTTCCGTAC	720
OY	751	acgttcgaagggggagaccaagctgtgaataaa	783
Db	721	ACGTTGGAAGGGGGGAGACCAAGCTTGAGATTA	753
RESULT	5		
LOCUS	XXUJ31739		
DEFINITION	XXUJ31739	864 bp	DNA
ACCESSION	U31739	Single chain antibody scA 13.1 gene, complete cds.	SYN
VERSION	U31739.1	GI:975304	05-SEP-1995
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
misc_feature			

Query Match	Best Local Similarity	Score	DB	Length
Matches 632; Conservative	78.3%; Pred. No. 1.6e-135;	482.6;	DB 12;	864;
	0; Mismatches 139; Indels 36; Gaps 3			
46	gcggcgatctctcccttgcggcggttcaactgcaagcgtctggggtgagctgtagg	105		
46	gcggcgatctctcccttgcggcggttcaactgcaagcgtctggggtgagctgtagg	105		
46	gcggcgatctctcccttgcggcggttcaactgcaagcgtctggggtgagctgtagg	105		
106	ccctggggtcctgagcgtctgcttcgcaaggtctggggtcctgagcgtcgtgagc	165		
106	ccctggggtcctgagcgtctgcttcgcaaggtctggggtcctgagcgtcgtgagc	165		
106	ccctggggtcctgagcgtctgcttcgcaaggtctggggtcctgagcgtcgtgagc	165		
166	atacactgggtgagcagaacaactgtgcaatggcctggaatgagctgagcgtgagc	225		
166	atacactgggtgagcagaacaactgtgcaatggcctggaatgagctgagcgtgagc	225		
166	atacactgggtgagcagaacaactgtgcaatggcctggaatgagctgagcgtgagc	225		
226	gaacactgtgtagctcctcaacaatcagaagttcaagaagcagcagcagcagcagc	285		
226	gaacactgtgtagctcctcaacaatcagaagttcaagaagcagcagcagcagcagc	285		
226	gaacactgtgtagctcctcaacaatcagaagttcaagaagcagcagcagcagcagc	285		
286	aaactcccaagcagaagcctacatgtagcgtccgcaagcctgagcagcagcagc	345		
286	aaactcccaagcagaagcctacatgtagcgtccgcaagcctgagcagcagcagc	345		
286	aaactcccaagcagaagcctacatgtagcgtccgcaagcctgagcagcagcagc	345		
346	tattactata-----aaatggttggagcctgggggccaagg	384		
346	tattactata-----aaatggttggagcctgggggccaagg	384		
346	tattactata-----aaatggttggagcctgggggccaagg	384		
385	actctgtagcagctctctcagagaggttaactcaca--gagatggctccgaatccaa	441		
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406	accacggctacacgcttccctcaggtgagagcggctttagcgagagaggtgctggc	465		
406	accacggctacacgcttccctcaggtgagagcggctttagcgagagaggtgctggc	465		
406	accacggctacacgcttccctcaggtgagagcggctttagcgagagaggtgctggc	465		
442	ccggaggatgtgtgtgtagcaccacaactcctcctgctctgcaagcttggagatcaa	501		
442	ccggaggatgtgtgtgtagcaccacaactcctcctgctctgcaagcttggagatcaa	501		
442	ccggaggatgtgtgtgtagcaccacaactcctcctgctctgcaagcttggagatcaa	501		

RESULT	6
LOCUS	XXU04796
DEFINITION	XXU04796 732 bp mRNA SYN 03-FEB-1996 Synthetic construct single-chain anti-acetylmethylcholine acetylcholinesterase mRNA, from PCR amplified mouse VH and VL regions, partial cds.
ACCESSION	U44786
VERSION	U44796.1 GI:1177222

SOURCE :	synthetic construct.
ORGANISM	synthetic construct.
REFERENCE	artificial sequence.
AUTHORS	1 (bases 1 to 732).
TITLE	Guesdon, J.-L. and Müller, B. H.
JOURNAL	Direct Submission
FEATURES	Submitted (05-JAN-1996) Jean-Luc Guesdon, Institut Pasteur, 28, rue du Docteur Roux, Paris, 75015, France
source	Location/Qualifiers
	1..732

	V_region	1..348	/note="heavy chain V(D)J region"
	misc_feature	1..23	/note="synthetic primer"
	CDS	<1..>732	/note="single-chain antibody"
		/codon_start=1	
		/transl_table=1	
		/product="soFv anti-acetylaminofluorene"	
		/protein_id="AA86761.1"	
		/db_xref="gi:1177223"	
		/translation="QVQLDQSGAEFLAKPGASVKRMSCKASGYTFRTYYMMHWYKORPQGQGLMIVYIDPTSTGYTYNQRFKDAITLPADSSSTAYVMQLSITSDSAVVYCARGSLTGVAGYWGQTITVTVSSGSGGGCGGGGGISLTGCPPELPSYLDDGSIAISRQSISLNNMTLRQPKGPSPLLIRYSNFRSEVLDRFGSGSGGTDFTKTSRVAEELKEIKR"	
misc_feature		325..418	
		/note="synthetic linker/primers"	
V_region		393..732	
		/note="light chain VJ region"	
BASE COUNT	186 a	182 c	199 g
ORIGIN			165 t

Query Match	57.4%;	Score 476.6;	DB 12;	Length 732;
Best Local Similarity	80.6%;	Pred. No. 1e-133;		
Matches 586;	Conservative	0;	Mismatches 129;	Indels 12;
			Gaps	2;

Oy	69	ggttcaacacgcagagagctctgggagctctggagctctggagctctgaagagctctc	128
Db	3	ggtagcagctgcagcagcagctctgggagctctgaacacgcaaaacctggggagctc	62
Oy	129	ctgcgaagctctgggctacacatttactgactatgaataaacctcgggtagagacac	188
Db	63	cttcaagagcttctggctctacaccttttacttacctctctctgagctctggtttaa	122
Oy	189	tgtgcattgcgcctggaatgtaattcctggatctatgtaacctgaactgtgtactg	248
Db	123	tggacacagggctctggaaatggaattggaatgcattgattccttactgtgtttat	182
Oy	249	tcgaagcttcaagagcaagagccatagtgaactgtagacaaacctccagacagc	308
Db	183	tcgaagcttcaagagcaagagccatagtgaactgtgacaaacctccagacagc	242
Oy	309	ggagctccgcagcccgaaatctggaagctctgctgccttacttactataag-----	359
Db	243	gcacactgcagcagcctgcgaattctgaagctctgcagctctgacagcttgcac	302
Oy	360	atggttttgagagctgggacaaaggagctctgtcactgtctctgca--gaggt	416
Db	303	atgcggaacactctggggcccaagagacacagctctccctctcctaagtgagc	362
Oy	417	ctcgaagatctgctccgaatcccaaccgggagatgtgtgatcagcccaaccac	476
Db	363	agcgcgaagctgctctggcggatggcggaatgggacatcgagctcactcagct	422
Oy	477	ccctgcctgcagctcttggagatacaagctccatctcttgcagatctagtcag	536
Db	423	ctgcctctgcagctcttggagatacaagctccatctcttgcagatctagtcag	482
Oy	537	acgaagtaatggaatccacttcttgaatcttgatctgcgcgagagcgaagc	596
Db	483	aaacagtaatggaatccacttcttgaatcttgatctgcgcgagagcgaagc	542
Oy	597	gctcttcgacttcaagaagttcccaacggaattcttggggtcccaagacaggt	656
Db	543	gctcttcgacttcaagaagttcccaacggaattcttggggtcccaagacaggt	602
Oy	657	tggataagaggaagatttccacatccaagatccaagagggaggttggaggt	716
Db	603	tggataagaggaagatttccacatccaagatccaagagggaggttggaggt	662
Oy	717	ttatttcgcttccaaatatacattgttcgtaacagcttgcaggagggagac	776
Db	663	ttatttcgcttccaaatatacattgttcgtaacagcttgcaggagggagac	722
Oy	777	ataaaaaa	783
Db	723	gctgcaaa	729

RESULT	7			
LOCUS	AF276797			
DEFINITION	AF276797	792 bp	mRNA	SYN
ACCESSION	AF276797			
VERSION	AF276797.1	GI:14279759		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				

Db	427	TTGATGATACCCAACTCCACTACTTTGTGCGTTACCATTTGGAAACAGACCTTCATCT	466
QY	514	ttgaagatctagtcagaagccttltacaagaatlgaaatcaactatltacatgtgtaactg	573
Db	487	TGCAGTCAAAGTCAGAGCCTCTGGATAGTGTAGGAAAAACATATTGTAATGGTGTGA	546
QY	574	cagaagaacgaagcccaagcttccaaagctccctatcttacaagtttcaaccgatttctggg	633
Db	547	CAGAGGCGAAGGGCAGCTCCCAAGCGCTATATCTAGTGTGTAAACTGTGACTCTGGA	606
QY	634	gtcccaagaaggtttcagtggaagtggatcagggaaagatttaacataagaatacaga	693
Db	607	GTCCCTGACAGGTTCATCTGGCAGTGGATCAGGGACAGATTTCACCTTTAAATCAACGA	666
QY	694	gttggaagcttgaaagatcttggaaatttcatlcttcgtcttcaagatagacatgttccgtacaa	753
Db	667	GTCGAGGCTGAGGATTTGGAGATTATTATTTGCTGGCAAGTACACATTCTCCGCTTACG	726
QY	754	ttcggagaggggagccaacgaactgtgaataataa	783
Db	727	TTGGGTGTGGTCAGCCAACTCGAAATTAAA	756

RESULT	9		PAT	06-MAR-1998
A59386				
LOCUS	A59386	749 bp	DNA	
DEFINITION	Sequence 36 from Patent WO9704092.			
ACCESSION	A59386			
VERSION	A59386.1	GI:3714722		

SOURCE	unidentified.
ORGANISM	unidentified.
REFERENCE	unclassified.
AUTHORS	1 (bases 1 to 749)
TITLE	Conseller,E. and Bracco,L.
JOURNAL	P53 PROTEIN VARIANTS AND THERAPEUTICAL USES THEREOF
COMMENT	Patent: WO 9704092-A 36 06-FEB-1997;
FEATURES	RHONE-POULENC RORER SA (FR)
source	Other publication FR 2736915 970124.
	Location/Ovalifiers
	1..749
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Query Match:	49.1%	Score 407.6:	DB: 6:	Length 749:
Best Local Similarity	74.1%	Pred. NO. 9.8e-113:		
Matches 347:	Conservative	0:	Mismatches 179:	Indels 12:
			Gaps 2:	
QY	58	gccttcgagcggttcaactgcagcaagcttgggctgcagctcgtgtgaagccttgggcttca	117	
Db	1	GCCTGCGCCCGAGTGTGCAGCTGCAGGAGCTAGGGCGACGCTTGTGGGTAGGGGCTCA	60	
QY	118	gtgcgcgtgtccctgcgaagcttcggagctcaacaattacttgactcttgaattacacttggt	177	
Db	61	GTCAGGTGTCCCTGCACACACTTCTTGCTTCAACATTATAAGCTCTATATGCACTGGGT	120	
QY	178	aggcagacacctgttcagctgcgcttgaattgatttgaagctatttgactcctgaactgttgt	237	
Db	121	AAGGAGGAGGCTTCAACAGGGCCTGAGGTGAGTGTGATGATTCCTGAGATGTGGAT	180	
QY	238	actgcctacacatagaagcttcaagcaagaagcgcacagctcttgaagcaaatccctcagg	297	
Db	181	ACTGAATATATCCCGGAGATTCACAGGGCAAGGCGACATATGACTGTGAGACACATCTCCAA	240	
QY	298	acagcctacaatgtgaagctccgcagcagctgtacatcttgaagaactctccgcgtctattacta	357	
Db	241	ACAACCTCACTCCAGCTGACGACGCTGGGATTTGAGGACCACTGGCGCTCTATTATTTGAAT	300	
QY	358	agat-----ggttcgagacctgtgggccaagaagactcgtgcctactgtctctcgagag	408	

Db	301	TTTTACGGGGATGCTTTTGGACTACTGGGGCCAAAGGACACAGGTCACCGTCTCCCTCAGGT	350
OY	409	ggttaaatccctca---ggaatctgctccgaatccaagaaccggagatctgtgtgaagccca	465
Db	361	GGAGCGGGTTTCAGGGCCGAGAGTGCTCTGGCGGTGGCGGATCGGATGGAATGTTTATGACCAA	420
OY	466	aaccacatcaccctgcctgttcaagctcttgagatccaagcctcgaatctcttgcagaatcagt	525
Db	421	ACGTCACTCACTTTGTCGGTTACCATTTGGAAACACAGCCCTCATCTCTTGCAGTCAAGT	480
OY	526	cagagccctttcacagtaatggaaatcaacctatttcatttgaatctgcagaaccagc	585
Db	481	CAGAGCCTCTTGTAAGATGATGGAAGAACAATATTTGAATGGTTGTTACAGAGCCACAGC	540
OY	586	cagttcccaagaagctctcgaatctacaagaattccaaccgaattctcgggtgtcccaagaag	645
Db	541	CAGCTCTCCAAAGCGCCTATATCTATCTGGTGTTCTTAAACTGAGACTCTGGAGTCCCTGGAAGG	600
OY	646	ttcagtcaggcagtcgatacgaagaaagattcaacctcaagatcaagaagaatggagctcga	705
Db	601	TTTCACTGCGCAGTGGATCAGGAGCAGATTTTCACTGAAATATCAAGAGGTGSAAGCTGAG	660
OY	706	gatacttggaatttattcttcgctctccaagtaagcacaatgtcttcgataacgtttcggaggggg	765
Db	661	GATTGGAGATTATTATGTGCGGCAAGGTACACAACTTCTCGGTCACGTTGGTGTCGGG	720
OY	766	accaagctcggaataataa 783	
Db	721	ACCAAGCTGGAGCTGAAA 798	

[illegible]

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	BASE COUNT	ORIGIN
420 a-	ggaatcgggtccgcgaatcaacaacccggagatgttgtgtatgaaccccaaccactctc	476											
363	AgGCGAGGAGTGGCTCTGGCGGTGGCGAGTGGATGTTTGTATGACCCAAATCCACAC	422											
477	ccctccgcgtacgtcttgagatcaagccctccatccctcttgacatctagctcagagccctt	536											
423	TTTGTGGTATACCATTTGGAAACCCACCCCTCATCTCTTGGCAAGTCAGTACGACCTCT	482											
537	acacagcgaatggaatcaacctattacatttgttacctgtcagaagccaggccagttccaa	596											
483	GGATAGTGAATGAAAAACATATTTGATTTGGTTTACAGAGGCGACGCCAGTCTCCAA	542											
597	gctccatcatcaaaagttcccaacgattttctgggtgcccaagagttcagttgacg	656											
543	GGCGCTATATATCTGTGTCTTAACCTGACACTCTGGATCTCCCTGACAGAGTTCACT	602											
657	tgtatcagggacagattcaacactcaagtcacagagatggaaggtcgaagatctggagt	716											
603	TGGATCAGGGAGACATTTCCACTTAAATTCACAGAGTGGAGGCTGAGATTGGGAGT	662											
717	ttattctgtctccaagtaacacatcttctgcacacctctggagggaggaacagctgga	776											
663	TTATTATGCTGGCAAGGTACACATCTCTCCGCTTACGTTGGTGTGTGACACAGCTGGA	722											
777	aataaa 783												
723	AATTAA 729												
RESULT 12													
LOCUS	A82599	1101 bp	DN										
DEFINITION	Sequence 1 from Patent WO9854312.												
ACCESSION	A82599												
VERSION	A82599.1	GI:6732343											
KEYWORDS													
SOURCE	unidentified.												
ORGANISM	unidentified.												
REFERENCE	1 (bases 1 to 1101)												
AUTHORS	He,M. and Tausaig,M.J.												
TITLE	RIBOSOME COMPLEXES AS SELECTION PARTICLES FOR IN VITRO DISPLAY AND												
JOURNAL	EVOLUTION OF PROTEINS												
FEATURES	Patent: WO 9854312-A.1 03-DEC-1998;												
FEATURES	BABRAHAM INST (GB); HE MINGYUE (GB)												
FEATURES	Location/Qualifiers												
FEATURES	1..1101												
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FEATURES	/db_xref="taxon:32644"												
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Best Local Similarity	73.2%;	Pred. No. 1.5e-109;											
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36	GSAGSTCMAROTCGASAGNCGWAGACTTGAGCTGAAGAAGCCTGGACAGACAGCTCAAGAT	95											
126	gtctctcaaggcttcgggtctaacacatttactgacta tgaataaacctggtgtgagggcag												

Qy	306	caatgagctccgaagcctgaacatctgaagaacctgcgcgtcttaactataaaga-----	360
Db	276	TTTTGGAGATCAACAACTCTCAAATATGAAACACGGCAACGATATTTCTCTTAAACAGGTGA	335
Qy	361	-----tggtttaggaactggggccaaggagactcgtgcaactgctctgcaga	407
Db	336	CTAGGTCACACTGGAGTACTGATGCTGTGGGGCCACAGGACACAGGTCAACGCTCTCTCAGC	395
Qy	408	gggttaaatcctcaaggatctggtctccgaatccaaccgggagatgtgtgatatgaccccaaa	467
Db	396	CAAAACGACACCCCACTCTGTATC-----CACTGGCCCAAGCTCGATGACCCAGAT	449
Qy	468	cccaactccctgcgtcagtccttgtagatcaaacctccatctcttgcaatctagta	527
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Qy	528	gaagccttttcaacagtaatgaaatccattcaacttggtaactgtcaagaagccaagcca	587
Db	510	GAGCGTTGTACACGATATGAGAAACACCTATTACATTTGTACCTGCAGAAAGCAGGCCA	569
Qy	588	gtcccaaaagctccgtgtatccaaagaatttccaaccgatttctgggggtcccaagcagtt	647
Db	570	GTCTCCAAAGTCTCTATCTACAAATTTCCAACCGATTTTATGGGGTCCACAGAGTT	629
Qy	648	caatggcagttgatacgaaggacagatttcaactcaagatcacagaagtgaagctgagga	707
Db	630	CAGTGCACAGTGAATCAAGGACAGATTTTCACACTCAAGATCACACACAGTGGAGGCTGAGA	689
Qy	708	tctggaggttaattatctgcgtccaaagatcacatgttccgtgaacggttcggaaggaggac	767
Db	690	TCTGGGATTTATTTTCGTCTCAAGTTCACATGTTCTCTCGAGGTTCCGTTGAGAGCAC	749
Qy	768	caagctggaataaaa	783
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DEFINITION	Sequence 2 from Patent WO9894312.	PAT	21-JAN-2000
ACCESSION	A82600		
VERSION	A82600.1	GI:6732344	
KEYWORDS			
SOURCE	unidentified.		
ORGANISM	unidentified		
REFERENCE	unclassified.		
AUTHORS	1 (bases 1 to 1103)		
TITLE	He, M. and Tauszig, M. J.		
JOURNAL	RIBOSOME COMPLEXES AS SELECTION PARTICLES FOR IN VITRO DISPLAY AND		
FEATURES	Patent: WO 9854312-A 2 03-DEC-1998;		
SOURCE	BABRAHAM INST (GB); HE MINQUE (GB)		
BASE COUNT	309 a	281 c	263 g
ORIGIN	245 t	5 others	
Query Match	47.98;	Score 397.2;	DB 6; Length 1103;
Best Local Similarity	73.2%;	Pred. No. 1.5e-109;	
Matches 539; Conservative	5;	Mismatches 168;	Indels 24; Gaps 2
Qy	66	ggcgggttcaactgcagcagctcggggtgagctggtgagggccttgaggcttaagcgt	125
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Qy	126	gtcctgcaaggcttcgggtacacatttactgaactgaataacatacactgggtgagcgac	185
Db	98	ctctccgaagccttctgggtatgcttcaaaaaatagtgaggaactggctgaagagac	157

QY 186 accgtgcatgagcctggaatgattgagcatatgctcctgaactgtgtgactgcta 245
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 QY 246 caatcaaaagtccaagacaagccatagatgactagacaatccctccagacagccta 305
 Db 218 TGTGTAGACTTCAAGGAGGAGTTTGCCCTTCTCTTGGAAACCTTGCCAGACAGCGCTA 277
 QY 306 catgagagctcgaagcctgacatctgaagactctgcgcgtcttactataaga----- 360
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 QY 361 -----tggtttagagctggggccaaagagactctggtacatgctctgcagca 407
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 QY 528 gagccttacaagataatgaatcacatcttactatgtaacctgcagaagccagagca 587
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 Db 692 TCTGGAAATTTATCTGTCTCTCAAAAGTTCCAGATGTTCTCGAGCCTGGTGGAGAGCA 751
 QY 768 caagctggaataaaa 783
 Db 752 CAAGCTGGAATTCAAA 767

RESULT 14
 LOCUS MMSCFVP25 795 bp mRNA ROD 13-JUN-1996
 DEFINITION Artificial mRNA for single chain antibody scfv (scfv25).
 ACCESSION 270662
 VERSION 270662.1 GI:1360013
 KEYWORDS heavy chain; light chain; single chain antibody; variable region.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 795)
 Fecker, L., Kaufman, A., Commandeur, U., Reither, J., Koenig, R. and
 Burgermeister, W.
 Expression of single chain antibody fragments (scfv) specific for
 beet necrotic yellow vein virus structural and nonstructural
 proteins in Escherichia coli and Nicotiana benthamiana
 unpublished
 2 (bases 1 to 795)
 Fecker, L.
 Direct Submission
 Submitted (03-APR-1996) Fecker L., Biologische Bundesanstalt fuer
 Land- und Forstwirtschaft, Institut fuer
 Biochemie/Pflanzenvirologi, Messeweg 11-12, Braunschweig, Germany,
 38-04

FEATURES
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BASE COUNT 195 a 208 c 222 g 170 t
 ORIGIN

Query Match 47.3%; Score 392.8; DB 10; Length 795;
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 Db 61 TCTGGCAAGCTTTGGTGTACACACTTTCTGCCATGAATACACTGGGTGAACAGCA 120
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 Db 181 AATCAGAAATTCAGAGGCAAGGCCACACTGACAGACAAATCCTCCAGCACACCTAC 240
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QY      760 ggggggacacaaagctcggaataaa-----agaagaaaacatctcccaagaagat 810
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QY      811 ctgaat 816
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RESULT 15
AF141321 738 bp mRNA ROD 01-JUN-1999
LOCUS     Mus musculus anti-VEE immunoglobulin single chain variable fragment.
DEFINITION
ACCESSION AF141321
VERSION    AF141321.1 GI:4929125
KEYWORDS   house mouse.
SOURCE     Mus musculus.
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 738)
AUTHORS   Alvi,A.Z., Stadnyk,L.L., Fulton,R.E., Nagata,L.P., Bader,D.E. and
            Suresh,M.R.
TITLE      Development of functional monoclonal single chain variable fragment
            antibody against Venezuelan equine encephalitis virus
JOURNAL    Unpublished
REFERENCE 2 (bases 1 to 738)
AUTHORS   Alvi,A.Z., Stadnyk,L.L., Fulton,R.E., Nagata,L.P., Bader,D.E. and
            Suresh,M.R.
TITLE      Direct Submission
JOURNAL    Submitted (07-APR-1999) Medical Countermeasures Section, Defence
            Research Establishment Suffield, P.O. Box 4000, Stn. Main, Medicine
            Hat, Alberta T1A 8K6, Canada
FEATURES   Location/Qualifiers
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BASE COUNT 184 a 181 c 206 g 167 t
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Best Local Similarity 74.1%; Pred. No. 2.9e-107;
Matches 548; Conservative 0; Mismatches 159; Indels 33; Gaps 3;
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Db 2 ttgcccagagtgcaactgacagcagctgagctgagctgagctgagctgagctgagctgag 61
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Db      122 AGACACCTGTGCATGGCTTAATGATTTGAGACTTTATATCTGTAACCTGGTGTACTG 181
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QY      302 cctacatgagagctccgagagctgacatctgaagagcttcgctcattactactaaga- 360
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QY      361 -----tggttgagagactggggccaaagagactctggtcactctctcgaag 406
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QY      407 aggttaaatcctca---ggaatcgtgctcgaatccaaacccgggagatgtctgtagacc 463
Db      362 GTGGAGGCGGTTCAAGCGGAGGTGCTGTGAGAGTTGCGGATCGGACATCGAGCTCAG 421
QY      464 caaacccacctccctcctgctcagctcgtcagctctgagagatcaagcctccatccttcgaatcta 523
Db      422 AGTCTCCAGCCTCCCTATCTGTATCTGTGTGGAGAAACTGTCAACCATCAATGTGACAGCA 481
QY      524 gtccagagctttacacagtaatggaatcaactattacattgtaactcctcgagagccag 583
Db      482 GTGAGAAATATT-----ACAGAAATTACCATGATATCAGCGAAACAGG 526
QY      584 gccagcttcaaaagctcctgactgactgactgactgactgactgactgactgactgactgact 643
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QY      644 gttcagctggaagtgatgacacagagagattccactcaagatcaagacagagtgagagctg 703
Db      587 GGTTCAGTGGGAGTGATGATCAGGACACAGATATTCCTCAAGATCAACACCTGAAAGTCTG 646
QY      704 agagctcggaggttattctgtctcgaagtagacatglttcgtagacgttcgagaggg 763
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: January 17, 2002, 23:54:57 ; Search time 110.25 Seconds
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Title: US-09-358-321c-31

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Gapop 10.0 , Gapept 1.0

Searched: 930621 seqs, 428652619 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	830	100.0	830	21	AA61047
2	528	63.6	828	21	AA61047
3	526.4	63.4	828	21	AA61047
4	521.4	62.8	819	21	AA61047
5	519.8	62.6	819	21	AA61047
6	510.8	61.5	876	19	AAV10390
7	501.2	60.4	1637	21	AA688358
8	499	60.1	753	20	AA677245
9	499	60.1	753	20	AA677241
10	476	57.3	753	22	AA670025
11	476	57.3	792	22	AA660021

Result No.	Score	Query Match	Length	DB ID	Description
12	447	53.9	459	21	AA61045
13	444	53.5	792	22	AA660022
14	443.4	53.4	786	22	AA660026
15	423.4	51.0	438	21	AA61046
16	419.4	50.5	1135	20	AA658936
17	415	50.0	1047	20	AA621156
18	415	50.0	1086	20	AA621158
19	411.6	49.6	768	17	AA648000
20	409.4	49.3	729	19	AA636236
21	408.2	49.2	753	21	AA61064
22	407.6	49.1	749	18	AA686234
23	405.2	48.8	1611	18	AA686221
24	401.4	48.4	726	20	AA686942
25	401.4	48.4	726	20	AA686943
26	397.2	47.9	1101	20	AA684663
27	397.2	47.9	1101	20	AA684663
28	393	47.3	782	16	AA686755
29	381.6	46.0	778	14	AA635955
30	381.6	46.0	925	21	AA658664
31	381.6	46.0	925	21	AA644206
32	380.4	45.8	772	14	AA635954
33	380.4	45.8	772	14	AA635954
34	368.8	44.4	879	19	AA631120
35	368.8	44.4	909	21	AA644235
36	368.8	44.4	918	21	AA644236
37	368.8	44.4	804	20	AA678155
38	367.8	44.3	747	22	AA630724
39	365.2	44.0	747	13	AA621098
40	364.2	43.9	726	22	AA624008
41	362.4	43.7	864	20	AA672072
42	361	43.5	723	19	AA610375
43	350	42.2	699	17	AA616700
44	350	42.2	1094	21	AA650982
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ALIGNMENTS

Result No.	Score	Query Match	Length	DB ID	Description
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5	519.8	62.6	819	21	AA61047
6	510.8	61.5	876	19	AAV10390
7	501.2	60.4	1637	21	AA688358
8	499	60.1	753	20	AA677245
9	499	60.1	753	20	AA677241
10	476	57.3	753	22	AA670025
11	476	57.3	792	22	AA660021

PI Sukhapinda K, Hasler JM, Petrell JK, Strickland JM, Folkerts C;
XX
XX
DR WPI: 2000-182711/16.
DR P-PSDB: AA68992.
XX
XX
Novel nucleic acid construct for down-regulating steady state levels of
PT proteins in plant cells, transgenic plants and their progeny -
PT
XX
PS Claim 21: Page 95-96; 114pp: English.

CC The present sequence encodes a single chain antibody which is
CC directed against a Zea mays (maize) delta9-desaturase. This sequence
CC is used to produce the constructs of the invention. These constructs
CC encode an antibody that can bind a transit peptide that directs an
CC associated passenger protein to a plant cell organelle. The transit
CC peptide sequence of the maize stearyl-ACP-delta9-desaturase
CC (delta9-desaturase) was determined, and used to produce antibodies
CC of the invention. These antibodies were produced in transgenic plants
CC of the invention. The constructs of the invention are useful for
CC producing antibodies which decrease steady state levels of passenger
CC proteins in the organelles of plant cells and plants, by binding to
CC the transit peptide. This results in the production of transgenic
CC plants which have altered steady state passenger protein levels.

Sequence 830 BP; 207 A; 200 C; 221 G; 202 T; 0 other;

Query Match	100.0%;	Score 830;	DB 21;	Length 830;
Best Local Similarity	100.0%;	Pred. No. 2.6e-225;		
Matches 830; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

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QY	61	ttgcggcggttcaacttgcagcagctctggggtcgcgcgtgtaagcctggggttcaatg	120
Db	61	ttgcggcggttcaacttgcagcagctctggggtcgcgcgtgtaagcctggggttcaatg	120
QY	121	acctctccgcgaagccttcggtgcacacattactatgactctgtaataacacctggtagg	180
Db	121	acctctctccgcgaagccttcggtgcacacattactatgactctgtaataacacctggtagg	180
QY	181	cagacacctgtgcattgaccttggtaatggatctggagctatgacctgtaaacctggtgact	240
Db	181	cagacacctgtgcattgaccttggtaatggatctggagctatgacctgtaaacctggtgact	240
QY	241	gcttaacaatcagaagctcagagagagagcgcacatgagactctgtagagcaaatctccagaca	300
Db	241	gcttaacaatcagaagctcagagagagagcgcacatgagactctgtagagcaaatctccagaca	300
QY	301	gcttacaatgtagagctccgcagccttgacatctgaaagactctgcgcgtctatcatatcacaga	360
Db	301	gcttacaatgtagagctccgcagccttgacatctgaaagactctgcgcgtctatcatatcacaga	360
QY	361	tgtgttggagagactcggggccaagggactctggtcactgtccttgaaagggttaattcctca	420
Db	361	tgtgttggagagactcggggccaagggactctggtcactgtccttgaaagggttaattcctca	420
QY	421	ggaatctggtccgaatcccaaacccgggggagtgtctgtagagaccacaacccactctccctg	480
Db	421	ggaatctggtccgaatcccaaacccgggggagtgtgtgtagagaccacaacccactctccctg	480
QY	481	ccgtgcagctcttggagatacaagagctcccatctcttgcagatctagtccagagcctttcac	540
Db	481	ccgtgcagctcttggagatacaagagctcccatctcttgcagatctagtccagagcctttcac	540
QY	541	agtaaatgtaacccatttaccatgtgtaaccgcgagaagcaggccagctcccaaacctc	600
Db	541	agtaaatgtaacccatttaccatgtgtaaccgcgagaagcaggccagctcccaaacctc	600
QY	601	ctgactacaagaatttccaacggaattctcgtgggtccagaagaagttcaatgtagatgga	660

Accession	Sequence	Length
Db	ctgactacaagaattccaacgcgattttctcgggtccacagacaggttcaagtcgacggtgga	660
QY	tcagggacagcagatttccacctccaaagatcaagcaagctcgagagctcgagagatcttcg	720
Db	tcagggacagcagatttccacctccaaagatcaagcaagctcgagagctcgagagatcttcg	720
QY	ttctgtctccaaagacacatgcttcgctaaagcttcgggggggagccaaagctcgaaata	780
Db	ttctgtctccaaagacacatgcttcgctaaagcttcgggggggagccaaagctcgaaata	780
QY	aaagaaagaaacatctctccagaaagagatctgaattgaagccggccg	830
Db	aaagaaagaaacatctctccagaaagagatctgaattgaagccggccg	830

RESULT	2
AAA92439	
ID	AAA92439 standard; DNA; 828 BP.

AC AAA92439;

DT 15-JAN-2001 (first entry)

DE	Plasmid pscM1 MABL1-scfv nucleotide sequence SEQ ID NO:20.
yy	

KW Monoclonal antibody; MABL; IAP; integrin associated protein;
single stranded EV; apoptosis; blood disease; leukemia;
KW

XX	cytostatic; ds.
KW	
XX	

OS	Mus
XX	sp

PN WO200053634-A1
XX

PD 14-SEP-2000:
XX

10-MAR-2000; 2000WC-JF01458.
XX

XX
XX

FN LO-MAH-1999; 390F-000333 / .

XX
XX
XX

(continued)

XXXXXXXXXXXX

[illegible]

DR P-PSDB; AAB23817.

PT Single stranded Fv antibody fragment inducing apoptosis in nucleated

PT	leukemia
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PS Example 5; Page 59-61; 73pp; Japanese.

The present invention describes a polypeptide containing the variable

CC apoptosis in nucleated blood cells having integrin-associated prote

CC (2) animal or microbial cells expressing the DNA of (1); and (3) agents for the treatment of blood disorders which contain the recombinant DNA

CC The polypeptide can be used in the treatment of blood disorders such as sickle cell anemia. The present sequence encodes the protein sequence for the polypeptide.

cc pscm1 MABLI-scfv, which is used in an example from the present invention

Sequence 828 RP: 211 A: 201 C: 223 G: 193 T: 0 Other: 0

Query Match	63.6%;	Score 528;	DB 21;	Length 828;
Best Local Similarity	82.9%;	Pred. No. 8.3e-140;		

```

matches 632; conservative 0; mismatches 113; indels 13; gaps 2,

```

Qy	46	gagcgacatctctcccttgcggcggtccacgtgacgacgttggcgcgagctgtgag	105
Db	46	gctgccaacgcgcacatggcgacgttccagctcagcaagcttgcacctgcacctgtlaag	105


```

Db 106 cctggcgtcctcagtgaaagatcctcgaaggcttcgttactcattcactgaataaac 165
QY 166 ataacctgggtgaagcagacacctgtcagtcgtgaatggattggaactttgacct 225
XX 166 atgacccgtgtgaagcagacagcagcagcagcagcagcagcagcagcagcagcagc 225
Db 226 gaaactgtgtgactgtcctcaatcagaagttcaaggacaaggcagcagcagcagcagc 285
QY 226 tactatgtgtgactgtcctcaatcagaagttcaaggacaaggcagcagcagcagcagc 285
Db 286 aatcccccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 345
QY 286 aatcccccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 345
Db 346 tattctgtgcaagatgagtgactagtgacgacgaggaaggccttactatgtttatgac 405
QY 346 gagggttaatcctcagatctgtgcgaatccaaacccgg-----ggatgttg 456
Db 406 ttctggggccaagggaccacggtcacccgtctcctcagcggggtgagcagatcgacatggag 465
QY 457 atgaccccaaacccactctcctgctgctgctgctgctgctgctgctgctgctgctgctgct 516
Db 457 atgaccccaaacccactctcctgctgctgctgctgctgctgctgctgctgctgctgctgct 516
QY 466 ctaactcagctcactcctcctgctgctgctgctgctgctgctgctgctgctgctgctgct 525
Db 517 agactctgctcagcagcctttacacagtaatgagtaactcattatgtgactgtcag 576
QY 526 agactctgctcagcagcctttacacagtaatgagtaactcattatgtgactgtcag 585
Db 577 aagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 636
QY 586 aagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 645
Db 637 ccaacacaggttcagtgagcagtgatcaggaagcagcagcagcagcagcagcagcagcagcagc 696
QY 646 ccagacacaggttcagtgagcagtgatcaggaagcagcagcagcagcagcagcagcagcagcagc 705
Db 697 gagcctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 756
QY 706 gagcctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 765
Db 757 ggaaggggggggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 804
QY 766 ggttgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 825
Db 805 gagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 837
QY 826 gagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 837

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PF 09-JUL-1999; 99WO-EP04838.
XX
PR 10-JUL-1998; 98EP-0112867.
XX
PA (CONN-) CONNEX GMBH.
XX
PI Reiter C;
XX
DR WPI; 2000-160926/14.
XX
DR P-PSDB; AAY78328.
XX
PT New oligonucleotide, polypeptide, antibody useful for treating
PT autoimmune disease, immune deficiencies, T-cell malignancies and
PT infectious diseases
XX
PS Example 9; Page 74; 79pp; English.
XX
CC The present invention describes a nucleic acid molecule (I) encoding at
CC least one complementary determining region (CDR) of a variable region of
CC an antibody which specifically interacts with the extracellular domain of
CC the human zeta-chain. The antibody whose CDR of a variable region is
CC encoded by (I), is obtained by immunising a rat with Jurkat cells and
CC subsequently with a conjugate comprising a carrier molecule and a
CC peptide having 11 N-terminal amino acids of a rat zeta-chain. The
CC anti-zeta-chain antibody is useful for the treatment and prevention of
CC autoimmune diseases, immune deficiencies, T-cell malignancies,
CC infectious diseases and the suppression of immune response preferably in
CC order to avoid graft rejection after organ transplantation, malignancies,
CC or viral infections. The antibody and fragments of it, can be useful for
CC the enhancement or suppression of NK-cell dependent immunity or for the
CC treatment of NK-cell derived malignancies. It can also be useful for the
CC differentiation of zeta-chain or eta-chain expression on NK-cells,
CC T-lymphocytes or their precursors. The present sequence encodes a
CC bispecific anti-zeta-chain/anti-EpCAM antibody, from an example from
CC
XX
SQ Sequence 1637 BP; 398 A; 404 C; 436 G; 399 T; 0 other;

```

Query Match 60.4%; Score 501.2; DB 21; Length 1637;
 Best Local Similarity 81.4%; Pred. No. 4,1e-133;
 Matches 619; Conservative 0; Mismatches 108; Indels 33; Gaps 2;

```

QY 57 tgccttgcggcgggttcaactcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 116
Db 810 tgccttgcggcgggttcaactcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 869
QY 117 agtgcagcttgcctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 176
Db 870 agtgcagcttgcctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 929
QY 177 gagcagacacccgtgcatgctgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 236
Db 930 gagcagacacccgtgcatgctgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 989
QY 237 tactgcataaactcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 296
Db 990 tactgcataaactcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1049
QY 297 cacagcctacatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 356
Db 1050 cacagcctacatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1109
QY 357 aagatgg-----ttggagcctggggcccaaggagc 386
Db 1110 aagcggggatcctcagatcactcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1169
QY 387 tctgtcactgtctctgca---gagggttaatcctcagatcgtgtccggaataaac 443
Db 1170 cagcgtacagctctccccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1229
QY 444 cgggagatgtgtgatgaccccaaacccactctcctgcgctgtcagcagcagcagcagcagcagcagc 503

```

Db 1230 ttctgagctcgtatgatacccaactccactctccctgctcgtcagcttggagatcaagc 1289
 QY 504 ctccactctctgagatactcaatcagaagcctttacaagaatgaatcacotatttaca 563
 Db 1290 ctccactctctgagatactcaatcagaagcctttacaagaatgaatcacotatttaca 1349
 QY 564 ttgttaccctgcaagaacccagagccagctcccaagctctctgatactcaagtttccaacg 623
 Db 1350 ttgttaccctgcaagaacccagagccagctcccaagctctctgatactcaagtttccaacg 1409
 QY 624 attctctgggtcccaagagaggttcagtgagtgatcaggagacagatttccacatca 683
 Db 1410 attctctgggtcccaagagaggttcagtgagtgatcaggagacagatttccacatca 1469
 QY 684 gatcagcagagtgagagctgagagatctggaggttatttctctcctcaagttacacatgt 743
 Db 1470 gatcagcagagtgagagctgagagatctggaggttatttctctcctcaagttacacatgt 1529
 QY 744 tccgtacacgttcggagggggagcagagctggaaataaa 783
 Db 1530 tccgtacacgttcggagggggagcagagctggagatcaaa 1569

RESULT 8

AAx77245
 ID AAX77245 standard; DNA; 753 BP.

XX AAX77245;

XX 04-AUG-1999 (first entry)

XX Mouse scfv fragment 4-7 encoding DNA.

XX Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
 KM autoimmune disease; scfv-antibody; single-chain Fv; mouse; ss.

XX Mus sp.

XX WO925818-A1.

XX 27-MAY-1999.

XX 16-NOV-1998; 98WO-EP07313.

XX 17-NOV-1997; 97EP-0120096.

XX (KUFE/) KUFER P.

XX Borschert K, Kufer P, Lutterbuese R, Raum T, Zettl F;

XX WPI: 1999-338004/28.

XX P-PSDB: AAY17962.

XX Phage display system for identification of binding site domains

XX retaining capacity to bind an epitope

XX Disclosure; Fig 6.8; 152pp; English.

XX The invention relates to a method of identifying binding site domains
 CC (BSD) that retain the capacity of binding to a predetermined epitope
 CC when positioned C-terminal of at least one further domain in a
 CC recombinant bi- or multivalent polypeptide. The method comprises (a)
 CC testing a panel of BSD displayed on the surface of a biological display
 CC system as part of a fusion protein for binding to a predetermined
 CC epitope, where the fusion protein comprises an additional domain
 CC positioned N-terminal of the BSD and an amino acid sequence that
 CC anchoring of the fusion protein to the surface of the display system;
 CC (b) identifying a BSD that binds to the predetermined epitope. The method
 CC is useful to identify bi- or multivalent polypeptides that comprise
 CC antibody binding sites capable of efficiently binding to the
 CC corresponding antigen. The polypeptides or antibodies identified by the
 CC method are useful therapeutically and diagnostically, for e.g. cancer and
 CC autoimmune diseases. scfv-antibody fragments that bind independently of

CC their position within bifunctional single-chain fusion proteins can be
 CC isolated from combinatorial antibody libraries using the new in vitro
 CC method. Sequences AAX7240-248 represent DNA sequences encoding mouse
 CC scfv fragments.
 XX
 SQ Sequence 753 BP; 171 A; 188 C; 215 G; 179 T; 0 other;

Query Match 60.1%; Score 499; DB 20; Length 753;
 Best Local Similarity 81.7%; Pred. No. 1,3e-131;
 Matches 615; Conservative 0; Mismatches 105; Indels 33; Gaps 2;

QY 64 ggcgcggttcaactgagacagatcctgggctggagccggtggagccctggggttcagtcagc 123
 Db 1 gaagtgcagctgctgcagacagctcgagagctggagccggtggagccctggggttcagtcagc 60
 QY 124 ctgtctcgaaggcttcgcggtctacacatttcaatgataatgatactggtgagggcag 183
 Db 61 ctgtctcgaaggcttcgcggtctacacatttcaatgataatgatactggtgagggcag 120
 QY 184 aacccgtgcatggtccttggaatggatgtgagctatgtatccccaagctggtgactggcc 243
 Db 121 aagcctggacaagctccttgagtgatggagaggttatacctagatctggttaagttac 180
 QY 244 tacaatcaagaagttcaagaagcagagccatagtgactgtagacaatactccccaagacagcc 303
 Db 181 tacaatgaagaagttcaagaagcagagccatagtgactgtagacaatactccccaagacagcc 240
 QY 304 tacatgagagctccgacagccttgacatctgaagacatctgcggtatattatatacaagaatgg 363
 Db 241 tccatgagagctccgacagccttgacatctgaagacatctgcggtatattatcttgagcaagaagg 300
 QY 364 -----ttgagagactggggccaaggacctcgtgctc 393
 Db 301 ggaatcccaagatacttaactaagacgtgtactctcgatgcttgggccaaggagacacagctc 360
 QY 394 actgtctctgca--gagggttaaatccccaagatctgtgctccgaatccaacccggagat 450
 Db 361 accgtctccctcagtggtgtgtgtcttgctggcggcgggctccggtgtgtgtgtc 420
 QY 451 gttgtgtgtgcccccaagccacatctccctcgtcgttgcagcttgagagtcagacacccctcagc 510
 Db 421 ctggtgagacccagacatccacatccctccgctgctgcaagcttgagagtcagacacccctcagc 480
 QY 511 tcttgagagatctagtcagagccttttacacagtaaatgaaatcaaccatttaccatgtgtac 570
 Db 481 tcttgagagatctagtcagagccttttacacagtaaatgaaatcaaccatttaccatgtgtac 540
 QY 571 ctgcagaagacccagccagcttccaaagctccctgatacttaagaagttccaacgatttct 630
 Db 541 ctgcagaagacccagccagcttccaaagctccctgatacttaagaagttccaacgatttct 600
 QY 631 ggggtcccaagacagttcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 690
 Db 601 ggggtcccaagacagttcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtc 660
 QY 691 agagtgagagctgagagatctggaggttatttctctgctcctcaagttacacatgttccgtac 750
 Db 661 agagtgagagctgagagatctggaggttatttctctgctcctcaagttacacatgttccgtac 720
 QY 751 acgttcgaggggggagcagagctggaaataaa 783
 Db 721 acgttcgaggggggagcagagctggagatcaaa 753

RESULT 9

AAx77241
 ID AAX77241 standard; DNA; 753 BP.

XX AAX77241;

XX 04-AUG-1999 (first entry)

XX

CC The recombinant monoclonal antibodies are useful in a passive
 CC immunity composition for contraception as they inhibit the ability of
 CC sperm to fertilize an egg. The antibodies may be used e.g. as an
 CC active ingredient of a spermstatic agent, or as a component of a
 CC spermicidal contraceptive.

XX Sequence 753 BP; 170 A; 191 C; 214 G; 178 T; 0 other;

Query Match 57.3%; Score 476; DB 22; Length 753;
 Best Local Similarity 80.0%; Pred. No. 4,2e-125;
 Matches 592; Conservative 0; Mismatches 130; Indels 18; Gaps 2;

QY 62 ttgcggcggttcaactgcagcagctgtggtgagctgtgagcctggggttcagtga 121
 DB 2 tggcccaagtgaaactgcagcagcctgtgacccggtgagcctggggttcagtga 61
 QY 122 cgtgtctctgcaagcttcggggtcaacatttactgtactatgaatacactgtgtgagc 181
 DB 62 aggtgtctctgcaagccttcgtgtcaacatttactgtactatgaatacactgtgtgagc 121
 QY 182 agacacctgtgcatgacctgtgaaatggtatgactatgtacctgaactgtgtgactgtg 241
 DB 122 agagcctgtgcaagcctgtgagctgtgagctgtgagctgtgagctgtgagctgtgagc 181
 QY 242 cctacaatcagaatgtcaagacaagccatagtgactgtgagcaaatcctccagcagc 301
 DB 182 actacagatgtgaatgtcaagacaagccatagtgactgtgagcaaatcctccagcagc 241
 QY 302 cctacaatgagctgtgagcctgtgacatctgaagactgtgacatctgaagactgtgagc 361
 DB 242 ttacatacaactgcagcagcctgtgacatctgaagactgtgacatctgaagactgtgagc 301
 QY 362 gg-----tttagagactggggcccaaggagactgtgacatctgtc---tg 403
 DB 302 gggactatgtgtgaccttgtttactgtgggccaaggccacacggtacacgttccagtg 361
 QY 404 cagaggtgaataatcctcaagatctgtgtccgaatccaaaccgggagatgtgtatgacc 463
 DB 362 gggggcgccgagcagctgt 421
 QY 464 caaacccactcctcctgctcctcagctgtgtgagatcaagcctccatctcttcagatcta 523
 DB 422 agtcccatctcctcctgctcctcagctgtgtgagatcaagcctccatctcttcagatcta 481
 QY 524 gtccagagccttttacaagatgaatgaatcacttttaccattgtgtacctgcagaagccag 583
 DB 482 gtccagagccttttacaagatgaatgaatcacttttaccattgtgtacctgcagaagccag 541
 QY 584 gccagcttcccaagctcctgtgtcttcaagaatgttccaaaccgaatttctgggggtccagaca 643
 DB 542 gccagcttcccaagctcctgtgtcttcaagaatgttccaaaccgaatttctgggggtccagaca 601
 QY 644 ggttcagtgagcagtgatcagggagacaatttcaacactcaagatcagcagaggtgtgagcgtg 703
 DB 602 ggttcagtgagcagtgatcagggagacaatttcaacactcaagatcagcagaggtgtgagcgtg 661
 QY 704 aggactgtgagatatttatttctgtctcgaagtatacattgttcggttaagcttgcgaagg 763
 DB 662 aggactgtgagatatttatttctgtctcgaagtatacattgttcggttaagcttgcgaagg 721
 QY 764 ggaaccaagctggaataaata 783
 DB 722 ggaaccaagctggaataaata 741

RESULT 11

AAF60021

ID AAF60021 standard; DNA; 792 BP.

XX AAF60021;
 XX 26-APR-2001 (first entry)

DE DNA encoding S19 scFv fragment and E tag.
 XX Antibody; S19; contraception; ds.
 XX Mus musculus.

PN W0200107083-A1.

PD 01-FEB-2001.

PF 21-JUL-2000; 2000MO-US19843.

PR 23-JUL-1999; 99US-0145512.

PA (UYVI-) UNIV VIRGINIA PATENT FOUND.

PI Herr JC, Norton ET, Diekmann AB;

DR WPI; 2001-182730/18.

PT New recombinant antibody derivative of monoclonal antibody S19, useful
 PT as a reagent for purifying or detecting human spermatozoa, as an active
 PT ingredient of a spermstatic agent, or as a component of a spermicidal
 PT contraceptive.

PS Claim 33; Page 39; 48pp; English.

CC The present invention relates to a recombinant antibody capable of
 CC specifically binding to sperm agglutination antigen-1 (SAGA-1).

CC The recombinant antibody has two peptide fragments of the S19

CC antibody and the fragments are joined together by a linker.

CC The recombinant monoclonal antibodies are useful in a passive

CC immunity composition for contraception as they inhibit the ability of

CC sperm to fertilize an egg. The antibodies may be used e.g. as an

CC active ingredient of a spermstatic agent, or as a component of a

CC spermicidal contraceptive.

Query Match 57.3%; Score 476; DB 22; Length 792;
 Best Local Similarity 80.0%; Pred. No. 4.3e-125;
 Matches 592; Conservative 0; Mismatches 130; Indels 18; Gaps 2;

QY 62 ttgcggcggttcaactgcagcagctgtggtgagcctgtgagcctggggttcagtga 121
 DB 2 tggcccaagtgaaactgcagcagcctgtgacccggtgagcctggggttcagtga 61
 QY 122 cgtgtctctgcaagcttcggggtcaacatttactgtactatgaatacactgtgtgagc 181
 DB 62 aggtgtctctgcaagccttcgtgtcaacatttactgtactatgaatacactgtgtgagc 121
 QY 182 agacacctgtgcatgacctgtgaaatggtatgactatgtacctgaactgtgtgactgtg 241
 DB 122 agagcctgtgcaagccttcgtgtcaacatttactgtactatgaatacactgtgtgagc 181
 QY 242 cctacaatcagaatgtcaagacaagccatagtgactgtgagcaaatcctccagcagc 301
 DB 182 actacagatgtgaatgtcaagacaagccatagtgactgtgagcaaatcctccagcagc 241
 QY 302 cctacaatgagctgtgagcctgtgacatctgaagactgtgacatctgaagactgtgagc 361
 DB 242 ttacatacaactgcagcagcctgtgacatctgaagactgtgacatctgaagactgtgagc 301
 QY 362 gg-----tttagagactggggcccaaggagactgtgacatctgtc---tg 403
 DB 302 gggactatgtgtgaccttgtttactgtgggccaaggccacacggtacacgttccagtg 361
 QY 404 cagaggtgaataatcctcaagatctgtgtccgaatccaaaccgggagatgtgtatgagcc 463
 DB 362 gggggcgccgagcagctgt 421

	QY	249	tcgaaagttcgaagggaaggaagggcgaatgagatctgtagagcaaatctctccagcaagagctacat	308
	Db	183	tcgaaagttcgaagggaaggaagggcgaatgagatctgtagagcaaatctctccagcaagagctacat	242
	QY	309	ggaagctccgaagctcgtaaatctgaagaactctgcgcgtctatactataaagatg-----	363
	Db	243	ccaactcgaagcagctgacatctgagactccgcggtctattactctgtaagaaggggacta	302
	QY	364	-----tttagaggaacttggggccaaggggaactctggtcaatgctc--tgcagaagg	410
	Db	303	tggttgcctcttctgtttacctggggccaagccacacggtccacggtcccaatggtgcgcg	362
	QY	411	taaatctcaagatcttgctctcggaatccaacccggggagtgtgtgatgaccccaaccc	470
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PA	(DOMC) DOM AGROSCIENCES LLC.			
PI	Sukhapiinda K, Hasler JM, Petell JK, Strickland JA, Folkerts O.			
XX	XX			

DR WPI: 2000-182711/16.
 DX P-PSDB; AAT68998.
 XX
 PT Novel nucleic acid construct for down-regulating steady state levels of
 PT proteins in plant cells, transgenic plants and their progeny
 XX
 PS Claim 21, page 94, 114pp; English.
 XX
 CC The present sequence encodes a variable region of the light chain
 CC of a monoclonal antibody which is directed against a Zea mays (maize)
 CC delta9-desaturase. The present sequence is used to produce the
 CC constructs of the invention. These constructs encode an antibody that
 CC can bind a transit peptide that directs an associated passenger protein
 CC to a plant cell organelle. The transit peptide sequence of the maize
 CC stearoyl-ACP delta9-desaturase (delta9-desaturase) was determined, and
 CC used to produce antibodies of the invention. These antibodies were
 CC produced in transgenic plants of the invention. The constructs of the
 CC invention are useful for producing antibodies which decrease steady
 CC state levels of passenger proteins in the organelles of plant cells
 CC and plants, by binding to the transit peptide. This results in the
 CC production of transgenic plants which have altered steady state
 CC passenger protein levels.
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 SQ Sequence 438 BP; 119 A; 108 C; 108 G; 103 T; 0 other;

Query Match:	51.0%	Score 423.4	DB 21:	Length 438:
Best Local Similarity	99.8%	Pred. No. 2.7e-110:		
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comphen Ltd.

CM nucleic - nucleic search, using sw model

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Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	380.4	45.8	772	1 US-08-331-398A-33	Sequence 33, Appl
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3	380.4	45.8	772	2 US-08-759-804A-33	Sequence 33, Appl
4	380.4	45.8	772	4 US-09-227-693-33	Sequence 31, Appl
5	349.2	42.0	741	4 US-09-227-693-31	Sequence 31, Appl
6	348.2	42.0	738	1 US-08-331-398A-31	Sequence 31, Appl
7	348.2	42.0	738	2 US-08-331-397B-31	Sequence 31, Appl
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10	338.8	40.8	814	2 US-08-752-844-65	Sequence 65, Appl
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27	316	38.1	537	5 PCT-US91-02942-2	Sequence 2, Appl

ALIGNMENTS

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RESULT 1
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; Sequence 33: Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David
; APPLICANT: Brickmann, Ulrich
; APPLICANT: Pal, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,398A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 772 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:

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33 311.6 37.5 720 2 US-08-800-198-7 Sequence 7, Appl
34 311.6 37.5 720 3 US-09-296-595-7 Sequence 7, Appl
35 311.2 37.5 2165 2 US-08-263-911-6 Sequence 6, Appl
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? OTHER INFORMATION: protein of B3 monoclonal antibody
? OTHER INFORMATION: Variable Heavy chain (V-H) and
? OTHER INFORMATION: Variable Light chain (V-L) Fv region
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? FEATURE:
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? LOCATION: 27..770
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; Sequence 33, Application US/08331397B

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1 Patent No. 5981726
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3 GENERAL INFORMATION:
4 APPLICANT: Pascan, Ita
5 APPLICANT: Benhar, Itai
6 TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
7 TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
8 TITLE OF INVENTION: thereof
9 NUMBER OF SEQUENCES: 68
10
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: Townsend and Townsend and Crew
13 STREET: One Market Plaza, Steuart Street Plaza
14 City: San Francisco
15 STATE: California
16 COUNTRY: USA
17 ZIP: 94105-1492
18
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Floppy disk
21 COMPUTER: IBM PC compatible
22 OPERATING SYSTEM: PC-DOS/MS-DOS
23 SOFTWARE: Patentin Release #1.0, Version #1.30
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/08/331,397B
26 FILING DATE: 28-OCT-1994
27 CLASSIFICATION: 435
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US 07/767,331
30 FILING DATE: 30-SEP-1991
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: US 07/596,289
33 FILING DATE: 12-OCT-1990
34 ATTORNEY/AGENT INFORMATION:
35 NAME: Hunter, Tom
36 REGISTRATION NUMBER: 38,498
37 REFERENCE/DOCKET NUMBER: 015280-1261200S
38 TELECOMMUNICATION INFORMATION:
39 TELEPHONE: (415) 543-9600
40 TELEFAX: (415) 543-5043
41 INFORMATION FOR SRO ID NO: 33:
42
43 SEQUENCE CHARACTERISTICS:
44 LENGTH: 772 base pairs
45 TYPE: nucleic acid
46 STRANDEDNESS: single
47 TOPOLOGY: linear
48 MOLECULE TYPE: DNA
49 FEATURE:
50 NAME/KEY: -
51 LOCATION: 1..772
52 OTHER INFORMATION: /note= "Single-chain antibody fusion
53 OTHER INFORMATION: protein of B3 monoclonal antibody
54 OTHER INFORMATION: Variable Heavy chain (V-H) and
55 OTHER INFORMATION: Variable Light chain (V-L) Fv region
56 OTHER INFORMATION: joined by a (Gly-4Ser)-3 peptide linker"
57 FEATURE:
58 NAME/KEY: CDS
59 LOCATION: 27..770
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CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourile and Crew
 STREET: Stewart Street Tower, One Market Plaza
 CITY: San Francisco
 STATE: California
 COUNTRY: US
 ZIP: 94105-1493
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
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 SOFTWARE: PatentIn Release #1.0, Version #1.25
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 FILING DATE:
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 APPLICATION NUMBER: US 07/767,331
 FILING DATE: 30-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/596,289
 FILING DATE: 12-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Ellen Lauver
 REGISTRATION NUMBER: 32,762
 REFERENCE/DOCKET NUMBER: 15280-126-1-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-5043
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 741 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
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 OTHER INFORMATION: B3(FV)"
 US-09-227-693-31

Query Match 42.08; Score 349; DB 4; Length 741;
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 Patent No. 5608039
 GENERAL INFORMATION:
 APPLICANT: Pastan, Ira
 APPLICANT: Willingham, Mark
 APPLICANT: Fitzgerald, David
 APPLICANT: Brinkmann, Ulrich
 APPLICANT: Pal, Lee
 TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
 NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew
 STREET: One Market Plaza, Stewart Street Plaza
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105-1492
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/331,398A
 FILING DATE: 28-OCT-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/767,331
 FILING DATE: 30-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/596,289
 FILING DATE: 12-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Hunter, Tom
 REGISTRATION NUMBER: 38,498
 REFERENCE/DOCKET NUMBER: 015280-1261100S
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043


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; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: "
; LOCATION: 1..738
; OTHER INFORMATION: /note= "Humanized B3 single-chain Fv"
;
US-08-759-804A-31

Query Match      42.0%; Score 348.2; DB 2; Length 738;
Best Local Similarity 69.5%; Pred. No. 2,6e-96;
Matches 511; Conservative 0; Mismatches 203; Indels 21; Gaps 2;

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QY      130 tgcagagcttcgggtctacacatttactgactatgaataacactggtgtgagcagacact 189
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QY      190 gtgcagagcctgagagatgagatgagctgagctgagctgagctgagctgagctgagct 249
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RESULT 11
US-08-403-853-17
; Sequence 17, Application US/08403853
; Patent No. 5844094
; GENERAL INFORMATION:
; APPLICANT: HUDSON, Peter J.
; APPLICANT: LAH, Maria
; APPLICANT: KORT, Alex A.
; APPLICANT: IRVING, Robert A.
; APPLICANT: ATWELL, John L.
; APPLICANT: MALBY, Robyn L.
; APPLICANT: POWER, Barbara E.
; APPLICANT: COLMAN, Peter M.
; TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,853
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU93/00491
FILING DATE: 24-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PL 4973
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/189/CHAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 831 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: mat-peptide
LOCATION: 1..819
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LOCATION: 1..819
US-08-403-853-17
Query Match 40.6%; Score 337.2; DB 2; Length 831;
Best Local Similarity 67.7%; Pred. No. 6e-93;
Matches 524; Conservative 0; Mismatches 208; Indels 42; Gaps 2;

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Search completed: January 18, 2002, 00:41:15
Job time: 2883 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 17, 2002, 23:48:02 ; Search time 1210.51 Seconds

(without alignments)
7367.966 Million cell updates/sec

Title: US-09-358-321c-31

Perfect score: 830

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372869281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 45 summaries

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20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	314.4	37.9	997	11	B1107100 602894523
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21	233.6	28.1	471	10	AA405772
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ALIGNMENTS

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LOCUS 602827925F1 NC1_CGAP_Co24 Mus musculus cDNA clone IMAGE:4982670 5',
DEFINITION
ACCESSION BG962941 GI:14350578
VERSION BG962941
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE
1 (bases 1 to 678)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNU)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNU at:
http://image.llnl.gov
Plate: L1AM10986 row: a column: 07
High quality sequence stop: 676.
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: oligo dT
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT      270 a      272 c      213 g      242 t
ORIGIN

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		/note="Organ: colon; Vector: pCMV-Sport6; Site:1. NOTI

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/clone_1b="NCI-CGAP_Cc24"
/lab_host="SH108 (TI phage-resistant)"
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Average insert size 1.6 kb. Constructed by Life

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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="UTGCM0041H23"

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ISSUE PROCUREMENT: GRIDER SMITH, P.H.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.

Email: cgapbs-r@mail.nih.gov

BASE COUNT	198 a	195 c	176 g	186 t
ORIGIN				

Email: cgapbs-ri@mail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1AM1369 row: k column: 04

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High quality sequence stop: 707.
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 /dex_stage="7 months"
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 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Robin Humphreys,
 NIH"

BASE COUNT 198 a 171 c 172 g 166 t
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Query Match

Best Local Similarity 33.3%; Score 276.4; DB 11; Length 707;
 Matches 326; Conservative 87.2%; Pred. No. 1,3e-68;
 Mismatches 46; Indels 2; Gaps 2;

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QY 470 caactcctcctgctcagctcgttgagagacaagctccatctcttcagatctagtcaga 529
    || || || || || || || || || || || || || || || || || || || || ||
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QY 530 gcccttacaacagtaatgaaatcaactatctggtacgtcagaagccagggccagt 589
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QY 590 ctccaaagctcctgctcaccagaagttccaccgagatttctgggggtcccaagagttca 649
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QY 650 gtggcagtgatcaggagacagatltcacactcaagatcagagagtgaggcttgaagatc 709
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DB 242 GTGGCAGTGATCAGGAGCAATTCACACCTCAGGGTCAAGAGTGAGGCTGAGGATC 301
QY 710 tgggaattatcttgcctcacaagataacatgttccgtacacgttcggagggggagcca 769
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DB 302 TGGAAGTTTATTACTGCTTCAAGGTCACATGTTCCCTACACGTTGAGAGGGGAGACA 361
QY 770 agctggaataaaaa 783
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Search completed: January 18, 2002, 00:16:31
 Job time: 1709 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 18, 2002, 00:40:07 ; Search time 43.97 Seconds

(without alignments)
453.166 Million cell updates/sec

Title: US-09-358-321c-32

Perfect score: 1391

Sequence: 1 MWSAIVLVLLAAAHSAFA.....FGGKLEKEKLEEDL 269

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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4: /SID2/gcgdata/geneseq/AA1982.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Match	Length	ID	Description
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3	984.5	70.8	274	AA168919	Plasmid psch2 MAB
4	978.5	70.3	271	AA168920	Plasmid psch2 MAB
5	963.5	69.3	274	AA168917	Plasmid psch2 MAB
6	957.5	68.8	271	AA168918	Plasmid psch2 MAB
7	944	67.9	532	AA178328	Bispecific anti-ze
8	943.5	67.8	251	AA178358	Mouse scfv fragmen
9	943.5	67.8	251	AA178358	Mouse scfv fragmen
10	927.5	66.7	252	AA178358	Mouse scfv fragmen
11	927.5	66.7	252	AA178358	Mouse scfv fragmen

RESULT	1	ALIGNMENTS
AA168992	AA168992 standard; Protein; 269 AA.	
AA168992	30-MAY-2000 (first entry)	
AA168992	Amino acid sequence of a single chain anti-delta9-desaturase antibody.	
AA168992	Delta9-desaturase; antibody; transmembrane protein; plant cell organelle; maize; stearyl-ACP-delta9-desaturase; transgenic plant.	
AA168992	Synthetic.	
AA168992	Mus sp.	
AA168992	Key	
AA168992	Protein	
AA168992	Location/Qualifiers	
AA168992	21..269	
AA168992	/note="mature protein"	
AA168992	MO200005391-A1.	
AA168992	03-FEB-2000.	
AA168992	21-JUL-1999; 99WD-US16405.	
AA168992	21-JUL-1998; 98US-0093587.	
AA168992	(DOWC) DOW AGROSCIENCES LLC.	
AA168992	Sukhinda K, Hasler JM, Petell JK, Strickland JA, Folkerts O,	
AA168992	WPI; 2000-182711/16.	

DR N-PSDB; AAZ61047.
 XX
 PT Novel nucleic acid construct for down-regulating steady state levels of
 PT proteins in plant cells, transgenic plants and their progeny
 XX
 PS Claim 22: Page 96-97; 114pp: English.
 XX
 CC The present sequence represents a single chain antibody which is
 CC directed against a Zea mays (maize) delta9-desaturase. The sequence
 CC is used to produce the constructs of the invention. These constructs
 CC encode an antibody that can bind a transit peptide that directs an
 CC associated passenger protein to a plant cell organelle. The transit
 CC peptide sequence of the maize stearyl-ACP-delta9-desaturase
 CC (delta9-desaturase) was determined, and used to produce antibodies
 CC of the invention. These antibodies were produced in transgenic plants
 CC or the invention. The constructs of the invention are useful for
 CC producing antibodies which decrease steady state levels of passenger
 CC proteins in the organelles of plant cells and plants, by binding to
 CC the transit peptide. This results in the production of transgenic
 CC plants which have altered steady state passenger protein levels.
 XX
 SQ Sequence 269 AA;
 Query Match 100.0%; Score 1391; DB 21; Length 269;
 Best Local Similarity 100.0%; Pred. No. 1,9e-100;
 Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVAATVYLVLLAAAHSAFAVQLQSGAELVRPGASVTLSCASGYTFDYEIHWRQT 60
 Db 1 mvaatlvylvllaaahsaafaavqlqsgaelvrpgasvtlscasgytfdyelhwrqt 60
 QY 61 PVHGLEMTGATDEPTGTAANOKFKDAITVCKSSSTAYMELRLSDSAVYYTTF 120
 Db 61 pvhglemtgatdeptgtatnqkfkdaivtckssstgmetrlstseavyyttrf 120
 QY 121 EDWOGTLVTVSAEGKSGSGSEKPGDVMVTPNPLSLPYSLDQASISCRSSQSLHSN 180
 Db 121 edwogtlvtvsaegksgsgsekpqdvmtvpnpplslpyslldqasiscrssqslhsn 180
 QY 181 GITYHMYLQKRGSGSKLLTYKVNRRSGVDRPFGSGSGTDTLTKISVEADLCVYFC 240
 Db 181 gitylmwyldkrgsgsklltykvnrrsgvdrpfsgsgsgtdtltkisveadlgyvfc 240
 QY 241 SQSTHVPYTFGGGTLEIKKEKLISEEDL 269
 Db 241 sqstlvpytfgggtlkeikekliseedl 269
 RESULT 2
 AAB09776
 ID AAB09776 standard; Protein: 267 AA.
 AC AAB09776;
 XX
 DT 06-SEP-2000 (first entry)
 XX
 DE TMV 30k movement protein and scFv fusion protein scFv 30-2 SEQ ID NO:30.
 XX
 KW Molecular pathogenicide; plant disease; resistance; antibody; scFv;
 KW gene construct; pathogen; toxin; fusion protein; antimicrobial;
 KW deoxyribonuclease; RNase; ribosome inactivator; immunomodulator.
 XX
 OS Tobacco mosaic virus.
 XX
 PN WO200023593-A2.
 XX
 PD 27-APR-2000.
 XX
 PF 15-OCT-1999; 99WO-EP07844.
 XX
 PR 16-OCT-1998; 98EP-0119630.
 PR 16-OCT-1998; 98IN-0000666.

XX
 PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
 XX
 PI Fischer R, Schillberg S, Naehring J, Sack M, Monecke M, Liao Y;
 PI Spiegel H, Zimmerman S, Emons N, Holzem A;
 XX
 DR WPI; 2000-339692/29.
 XX
 PT New fusion proteins and gene constructs for expressing agents
 PT (antibodies, enzymes, vectors or molecular pathogenicides), useful for
 PT protecting plants against pathogens and increasing resistance to
 PT disease
 XX
 PS Example 5; Page 150-151; 193pp: English.
 XX
 CC The present invention describes a fusion protein (I) comprising at least
 CC one binding domain specifically recognising an epitope of a plant
 CC pathogen and at least one further domain comprising a protein or peptide
 CC sequence which is toxic to the pathogen or detrimental to its
 CC replication, transmission or life cycle. Also described is a
 CC pathogenicide (II) comprising (I) and a cellular targeting sequence
 CC and/or membrane localisation sequence and/or motif that leads to
 CC membrane anchoring; or at least one binding domain that specifically
 CC recognises a viral movement and/or replicase protein. The fusion
 CC protein, pathogenicide, polynucleotide, vectors, and compositions from
 CC the present invention are useful for the protection of a plant against
 CC the action of a pathogen. The kit from the present invention is useful
 CC for carrying out the methods and may be employed in different
 CC applications, for example in the diagnostic field or as research tools.
 CC The kit or its components, such as the fusion protein, pathogenicide,
 CC polynucleotides, vectors or compositions are useful in plant cell and
 CC plant tissue culture, in agriculture. They are extremely useful for
 CC breeding new varieties of plants that display improved properties such as
 CC resistance to pathogens. AAs5687 to AAs5702 and AAB09774 to B097820
 CC represent sequences used in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 267 AA;
 Query Match 71.2%; Score 990; DB 21; Length 267;
 Best Local Similarity 74.4%; Pred. No. 2.5e-69;
 Matches 195; Conservative 21; Mismatches 32; Indels 14; Gaps 3;
 QY 22 VOLQSGAELVRPGASVTLSCASGYTFDYEIHWRQTPVHGLEMTGATDEPTGTA 81
 Db 2 vqlqsgaelvrpgasvtlscasgytfdyelhwrqtpvhglemtgatdeptgtatn 81
 QY 82 OKFKDAITVVDKSSSTAYMELRLSDSAVYY-----YTRWEDMGCGTLTVVSAEG 135
 Db 82 okfkdaivtvdkssttaymrlstseavyy-----ytrwfdmgcgtlvvssag 121
 QY 136 KSSGSGSEKPG-DVMTNPNPLSLPYSLDQASISCRSSQSLHSNGITYLHMYLQKRGQ 194
 Db 136 kssgsgsekpq-dvmtvpnpplslpyslldqasiscrssqslhsngitylmwyldkrg 181
 QY 195 SPKLLITKVNRRSGVDRPFGSGSGTDTLTKISREADLDVYRCSTHRYPTFFGGGT 254
 Db 195 spkllitkvnrrsgvdrpfsgsgsgtdtltkisreaddlvyrctshryptffgggt 241
 QY 255 KLEIK-----EKKLISEEDL 269
 Db 255 kleikvadaaeeqkliseedl 263
 RESULT 3
 AAB23819
 ID AAB23819 standard; Protein: 274 AA.
 XX
 AC AAB23819;
 XX
 DT 15-JAN-2001 (first entry)
 XX

```

DE Plasmid pscw2 MABL2-scfv protein sequence SEQ ID NO:24.
KW Monoclonal antibody; MABL; IAP; integrin associated protein;
XX single stranded Fv; apoptosis; blood disease; leukaemia;
KM cytosolic.
CS Mus sp.
OS W0200053634-A1.
PD W0200053634-A1.
PF 14-SEP-2000.
PI 10-MAR-2000; 2000WO-JP01458.
PR 10-MAR-1999; 99JP-0063557.
PS (CHUS ) CHUGAI SEIYAKU KK.
XX Fukushima N, Uno S;
XX WIPI: 2000-587428/55.
XX DR N-PDSB; AAA82443.
XX Single stranded Fv antibody fragment inducing apoptosis in nucleated
PT leukemia having integrin associated protein for treatment of
PT leukemia -
XX Example 5; Page 64-66; 73pp; Japanese.
XX The present invention describes a polypeptide containing the variable
CC region of the light chain of a monoclonal antibody, which induces
CC apoptosis in nucleated blood cells having integrin associated protein
CC (IAP). Also described are: (1) DNA encoding the novel polypeptide;
CC (2) animal or microbial cells expressing the DNA of (1); and (3) agents
CC for the treatment of blood disorders which contain the polypeptide.
CC The polypeptide can be used in the treatment of blood disorders such
CC as leukemia. The present sequence represents the protein sequence from
CC pscw2 MABL2-scfv, which is used in an example from the present
XX invention.
XX Sequence 274 AA:
SQ
Query Match 73.8%; Score 984.5; DB 21; Length 274;
Best Local Similarity 76.0%; Pred.No.7e-69;
Matches 196; Conservative 16; Mismatches 41; Indels 5; Gaps 2.
QY 10 LLAATAASARAFAAQLGSGAEIVRPGASVLTSCKASGYFTDYEIHVVROTPVHGLEWIG 69
Db 12 llllaagpanaqgqlqgsdpelvkpgasvkmccksgyftanhhvwkkgpggglewlg 71
QY 70 AIDPETGGTLYNNOKFEKDAIVTDKSSSTAYVELRLSLTSDSAVYYTR---WFEDMGQ 125
Db 72 ylypyngdgtkynekikdkatlttsckastlaymdlsslsedsavycargyytlyddwgq 131
QY 126 GTITVTAAEKKSSGSSSESERPG-DVMMPNPLSLVSIGDDASTSCSSSGLHSNGITY 184
Db 132 gtlctvsaggsgsgggsgggsgdvmtcspislpsvlsgdqaslscrssgslvhmgkly 191
QY 185 LHMVLOKPGQSFKLLIYKVSNRPSPGVDFRFSGSGTDFTLTKISRVPAEDLGVFQCOST 244
Db 192 lhmvlgkpqgsprklilyksnrntfsgypdfstfgsvtdflmistrveedilgyvfcsqst 251
QY 245 HVPTFGCGTKLEKEEK 262
Db 252 hvpytfgggtkleikdyk 269
RESULT 4
AAAB23820
XX ID AAB23820 standard; Protein; 271 AA.
AC AAB23820;
```

```
DT      XX 15-JAN-2001    (first entry)
DE       DE Plasmid pCHOM2 MABL2-scfv protein sequence SEQ ID NO:25.
XX       KM Monoclonal antibody; MABL; IAP; integrin associated protein;
KM single stranded FV; apoptosis; blood disease; leukaemia;
KW cytostatic.
OS Mus sp.
PN WO200053634-A1.
PD 14-SEP-2000.
PF 10-MAR-2000; 2000WO-JP01458.
PR 10-MAR-1999; 99CP-0065557.
PA (CHUS ) CHUGAI SEIYAKU KK.
PI Fukushima N, Uno S;
XX WPI , 2000-587428/55.
DR N-PDBB ; AAA92444.
XX CC The present invention describes a polypeptide containing the variable
PS CC region of the light chain of a monoclonal antibody, which induces
CC apoptosis in nucleated blood cells having integrin associate protein
CC (IAP). Also described are: (1) DNA encoding the novel polypeptide;
CC (2) animal or microbial cells expressing the DNA of (1); and (3) agents
CC for the treatment of blood disorders which contain the polypeptide.
CC The polypeptide can be used in the treatment of blood disorders such
CC as leukemia. The present sequence represents the protein sequence from
CC pcHOM2 MABL2-scfv, which is used in an example from the present
XX invention.
SQ Sequence          271 AA:

Query Match              70.3%; Score 978.5; DB 21; Length 271;
Best Local Similarity   74.0%; Pred. No. 2e+68;
Matches 199; Conservative 19; Mismatches 43; Indels 7; Gaps 3,

OY     3 SAIVLYLLAAAHSAFAAVQLQSGAELVRGASVTITSCKASYTTTDEVETHWKOTPY 62
Dd     4 scilIF-lvalatlgdsqvqlqgspeivrpgasvkmsckasytlanhvllwvxkbp9 61
OY     HGLEWICAIIDPETGGTAAYNOKFKDKAITVVKSSSTIAEMRLSJTSEDSAWYYTR---- 118
Db     62 gglewlaiylypyndgfkkynekfkdakaltsdstetamldtsiasedsavyycaargyv 121
OY     119 WFEDMGOGTLVTVSAEGKSQSGSESKEPG-DVMTPNFSLSPVLSGDQASISGRSSQSGL 177
Db     122 tyddwgaggtclltvsrgggsggsgggsgsdvmtgbplslpvallgdgaaiscrrssglv 181
OY     178 HSNGITATLVHYLOKPOGPSKLILYVSNSFSGVPREFGSGSDGFPLKTSRYAEADLGV 237
Db     182 hsngrkylhmajlkpqspsklilykvnsrfsysvpairsysgvrdftcmstveeedlgy 241
OY     238 YFCGSOSTHPVPTFGGCTKLEIKEEK 262
Db     242 yfcsgshypytfggtklrkdkyk 266
```

RESULT_5
TAB23817

ID AAB23817 standard; Protein; 274 AA.
XX
AC AAB23817;
XX
DT 15-JAN-2001 (first entry)
XX
DE Plasmid pCHO1 MAB1-scFv protein sequence SEQ ID NO:20.
XX
KW Monoclonal antibody; MAB1; IAP; integrin associated protein;
KW single stranded Fv; apoptosis; blood disease; leukemia;
KW cytosolic.
XX
OS Mus sp.
XX
PN WO200053634-A1.
XX
PD 14-SEP-2000.
XX
PF 10-MAR-2000; 2000WO-JP01458.
XX
PR 10-MAR-1999; 99JP-0063557.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Fukushima N, Uno S;
XX
DR WPI: 2000-587428/55.
DR N-PSDB: AAA92439.
XX
PT Single stranded Fv antibody fragment inducing apoptosis in nucleated
PT blood cells having integrin associated protein for treatment of
PT leukemia -
XX
PS Example 5; Page 59-61; 73pp: Japanese.
XX
CC The present invention describes a polypeptide containing the variable
CC region of the light chain of a monoclonal antibody, which induces
CC apoptosis in nucleated blood cells having integrin associate protein
CC (IAP). Also described are: (1) DNA encoding the novel polypeptide;
CC (2) animal or microbial cells expressing the DNA of (1); and (3) agents
CC for the treatment of blood disorders which contain the polypeptide.
CC The polypeptide can be used in the treatment of blood disorders such
CC as leukemia. The present sequence represents the protein sequence from
CC pCHO1 MAB1-scFv, which is used in an example from the present
CC invention.
XX
SQ Sequence 274 AA;

Query Match 69.3%; Score 963.5; DB 21; Length 274;
Best Local Similarity 74.8%; Pred. No. 3e-67;
Matches 193; Conservative 15; Mismatches 45; Indels 5; Gaps 2;
XX
QY 10 LLAHAHSAFAAVOLQSGAEIVPGASVTLSCKASGYTFDYEIMHWKOTPVHGLEWIG 69
DB 12 LLLAAGAMAGVQLGSGPDLVPGASVTKMSCKASGYTLVNHVHWKQPGGLGWI 71
QY 70 AIDPTGCTAVNQKFKDKAIVTVDKSSSTAYMELRSLTSDSAVYYTRM---FEDWQ 125
DB 72 YIYPNDGTLKYNEKFKGKATLSEKSSAAAMELSASEDSAAVYCARGYYSYDDWQ 131
QY 126 GTLVVSAEKKSSGSGSEKPG-DVYMTFNPPLSLPVSLGQASISCRSSQSLHSGITY 184
DB 132 GTLTIVSAGGSG 191
QY 185 LHWLQKPGSPKLLIYKVSNRFGVDFRSGSGSGTFTLKISRVEADLGYVFCQSQT 244
DB 192 LGWYQKPGSPKLLIYKVSNRFGVDFRSGSGSGTFTLKISRVEADLGYVFCQSQT 251
QY 245 HVPYTFGGGCTLEIKKK 262
DB 252 HVPYTFGGGCTLEIKKK 269

RESULT 6
ID AAB23818 standard; Protein; 271 AA.
XX
AC AAB23818;
XX
DT 15-JAN-2001 (first entry)
XX
DE Plasmid pCHO1 MAB1-scFv protein sequence SEQ ID NO:23.
XX
KW Monoclonal antibody; MAB1; IAP; integrin associated protein;
KW single stranded Fv; apoptosis; blood disease; leukemia;
KW cytosolic.
XX
OS Mus sp.
XX
PN WO200053634-A1.
XX
PD 14-SEP-2000.
XX
PF 10-MAR-2000; 2000WO-JP01458.
XX
PR 10-MAR-1999; 99JP-0063557.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Fukushima N, Uno S;
XX
DR WPI: 2000-587428/55.
DR N-PSDB: AAA92442.
XX
PT Single stranded Fv antibody fragment inducing apoptosis in nucleated
PT blood cells having integrin associated protein for treatment of
PT leukemia -
XX
PS Example 5; Page 62-64; 73pp: Japanese.
XX
CC The present invention describes a polypeptide containing the variable
CC region of the light chain of a monoclonal antibody, which induces
CC apoptosis in nucleated blood cells having integrin associate protein
CC (IAP). Also described are: (1) DNA encoding the novel polypeptide;
CC (2) animal or microbial cells expressing the DNA of (1); and (3) agents
CC for the treatment of blood disorders which contain the polypeptide.
CC The polypeptide can be used in the treatment of blood disorders such
CC as leukemia. The present sequence represents the protein sequence from
CC pCHO1 MAB1-scFv, which is used in an example from the present
CC invention.
XX
SQ Sequence 271 AA;

Query Match 68.8%; Score 957.5; DB 21; Length 271;
Best Local Similarity 72.8%; Pred. No. 8.6e-67;
Matches 193; Conservative 18; Mismatches 47; Indels 7; Gaps 3;
XX
QY 3 SAIVLYVLLAAHSAFAAVOLQSGAEIVPGASVTLSCKASGYTFDYEIMHWKOTPV 62
DB 4 SCILLF--IYATATGYDSGVLGSGPDLVPGASVTKMSCKASGYTLVNHVHWKQPG 61
QY 63 HGLEWIGAIIDPTGCTAVNQKFKDKAIVTVDKSSSTAYMELRSLTSDSAVYYTRM--- 119
DB 62 GGLIEWIYIYPYNDGTLKYNEKFKGKATLSEKSSAAAMELSASEDSAAVYCARGY 121
QY 120 -FEDWQGTIVVSAEKKSSGSGSEKPG-DVYMTFNPPLSLPVSLGQASISCRSSQSL 177
DB 122 SYDGGVGTTLTVSAGGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 181
QY 178 HSNGITLHWYLOKPGSPKLLIYKVSNRFGVDFRSGSGSGTFTLKISRVEADLGY 237
DB 182 HSKGNTLYQWYQKPGSPKLLIYKVSNRFGVDFRSGSGSGTFTLKISRVEADLGY 241
QY 238 YFCQSQTHVPTFGGCTLEIKKK 262


```

Query Match      67.8%; Score 943.5; DB 20; Length 251;
Best Local Similarity 75.7%; Pred. No. 9, 6e-66;
Matches 187; Conservative 13; Mismatches 36; Indels 11; Gaps 2;

QY 24 LQSGAELVRPGASVTLSCKASGYTFDYERHWRQTPVHGLEWIGALDPETGTAAYNQK 83
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 5 legsgaelvrpgasvtlscckasgytlcsyglswkxqrltgglawelgvprlgnaynek 64
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 84 FKDKAIVTVDKSSSTAYNELRSLTSDSAVY-----YTRMFEDMGGLTVYSA 133
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 65 fkgakltadkssstaemrlstsedavyfcarrgsydlnydwylfwvggltvts 124
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 134 EGKSSGSGSESKPG-DVYVMPNPLSLPVSLGDQASISCRSSQSLHNSGITYLHWYLOKP 192
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 125 gggsgsgsgsgsgselvmtqrlpslpslqdgasiscrsqslvhsngntylhwylqkp 184
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 193 GQSPKLLIYKVSNNRFGVPRFRSGSGSDFTLKISFVEADLGVYFCQSSTHVPYTFGG 252
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 185 gqspklllykvsnrfsqprdfsgsgsgtdftlklsrveadlgyvfcsqsthyptfsg 244
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 253 GTKLEIK 259
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 245 gtlkleik 251
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 9
AAI17962
ID AAI17962 standard; Protein; 251 AA.
XX
AC AAI17962;
XX
DT 04-AUG-1999 (first entry)
XX
DE Mouse scfv fragment 4-7.
XX
KW Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
KW autoimmune disease; scfv-antibody; single-chain Fv; mouse.
XX
OS Mus sp.
XX
PN W09925818-A1.
XX
PD 27-MAY-1999.
XX
PR 16-NOV-1998; 98WC-EP07313.
XX
PR 17-NOV-1997; 97EP-0120096.
XX
PA (KUFE/) KUFER P.
XX
PI Borschert K, Kufer P, Lutterbuese R, Raum T, Zettl F;
XX
DR WPI; 1999-338004/28.
XX
DR N-PSDB; AAX71245.
XX
PT Phage display system for identification of binding site domains
XX
PS retaining capacity to bind an epitope
XX
PS Claim 27; Fig 6.8; 152pp; English.
XX
XX
The invention relates to a method of identifying binding site domains
(CC BSD) that retain the capacity of binding to a predetermined epitope
(CC when positioned C-terminal of at least one further domain in a
(CC recombinant bi- or multivalent polypeptide. The method comprises (a)
(CC testing a panel of BSD displayed on the surface of a biological display
(CC system as part of a fusion protein for binding to a predetermined
(CC epitope, where the fusion protein comprises an additional domain
(CC positioned N-terminal of the BSD and an amino acid sequence that mediates
(CC anchoring of the fusion protein to the surface of the display system; and
(CC (b) identifying a BSD that binds to the predetermined epitope. The method
(CC is useful to identify bi- or multivalent polypeptides that comprise
(CC antibody binding sites capable of efficiently binding to the

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CC corresponding antigen. The polypeptides or antibodies identified by the
CC method are useful therapeutically and diagnostically, for e.g. cancer and
CC autoimmune diseases. scfv-antibody fragments that bind independently of
CC their position within bifunctional single-chain fusion proteins can be
CC isolated from combinatorial antibody libraries using the new in vitro
CC method. Sequences AAI17957-965 represent mouse scfv fragments.
XX
SQ Sequence 251 AA:
XX
Query Match      67.8%; Score 943.5; DB 20; Length 251;
Best Local Similarity 75.7%; Pred. No. 9, 6e-66;
Matches 187; Conservative 14; Mismatches 35; Indels 11; Gaps 2;

QY 24 LQSGAELVRPGASVTLSCKASGYTFDYERHWRQTPVHGLEWIGALDPETGTAAYNQK 83
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 5 legsgaelvrpgasvtlscckasgytlcsyglswkxqrltgglawelgvprlgnaynek 64
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 84 FKDKAIVTVDKSSSTAYNELRSLTSDSAVY-----YTRMFEDMGGLTVYSA 133
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 65 fkgakltadkssstaemrlstsedavyfcarrgsydlnydwylfwvggltvts 124
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 134 EGKSSGSGSESKPG-DVYVMPNPLSLPVSLGDQASISCRSSQSLHNSGITYLHWYLOKP 192
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 125 gggsgsgsgsgsgselvmtqrlpslpslqdgasiscrsqslvhsngntylhwylqkp 184
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 193 GQSPKLLIYKVSNNRFGVPRFRSGSGSDFTLKISFVEADLGVYFCQSSTHVPYTFGG 252
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 185 gqspklllykvsnrfsqprdfsgsgsgtdftlklsrveadlgyvfcsqsthyptfsg 244
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 253 GTKLEIK 259
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 245 gtlkleik 251
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 10
AAW02279
ID AAW02279 standard; Protein; 252 AA.
XX
AC AAW02279;
XX
DT 29-OCT-1996 (first entry)
XX
DE 26-10 anti-digoxin two single chain Fv construct.
XX
XX
26-10; anti-digoxin; monoclonal antibody; single chain Fv; scfv;
KW construct; C-terminal amino acid sequence; in vivo imaging;
KW drug targeting experiment; homodimer.
XX
XX Homo sapiens.
XX
OS
XX
FH Key Location/Qualifiers
XX Peptide 248..252
XX FT /note="Claimed C-terminal tail to facilitate
XX crosslinking of two scfv polypeptides"
XX
XX US5534254-A.
XX
XX 09-JUL-1996.
XX
XX 06-FEB-1992; 92US-0831967.
XX
XX 07-OCT-1993; 93US-0133804.
XX 06-FEB-1992; 92US-0831967.
XX
XX (CHIR ) CHIRON CORP.
XX (CREA-) CREATIVE BIOMOLECULES INC.
XX
XX Houston LL, Huston JS, Oppermann H, Ring DB;
XX WPI; 1996-333194/33.
XX
XX N-PSDB; AAT36879.
XX

```


PT	Compsn contig, antigen-targetting antibody fragment constructs	
XX	comprising dimer of single-chain Fv fragments	
PS	Example 1: Columns 29-32: 30pp: English.	
CC	Construction of the anti-digoxin 26-10 single chain Fv is described	
CC	in full in US5091513, briefly the sythetic gene was constructed	
CC	by ligating multiple synthetic DNA duplexes. A synthetic DNA duplex	
CC	encoding the C-terminal amino acid sequence, (Gly)4-Cys was	
CC	inserted, and the resulting sfv inserted into an expression vector.	
CC	The resulting gene, which encodes the present sequence, was	
CC	transformed into E. coli, and protein expression induced by the	
CC	addn. of IPTG to the culture medium. A compsn. comprising a carrier	
CC	and the sfv protein prod. can be used for in vivo imaging, and drug	
CC	targetting experiments.	
XX		
SQ	Sequence 252 AA:	
Query Match	66.7%; Score 927.5; DB: 17; Length 252;	
Best Local Similarity	76.6%; Pred. No. 1,7e-64;	
Matches 187; Conservative 17; Mismatches 33; Indels 7; Gaps		
OY	22 VOLDQSAELVPCGASVTLSCNAGSYTFDDYELHWRQTPVHGLEWIGALIDPETGTAYN 81	
Db	3 VQLQSGPELVKPGASVRLMSCKSSGYIFDFYMANVTRSGHSLDYLISLPYSGVGYGN 62	
OY	82 GKFEKRLIVVDKSSSAVYELRLSEDSAYYY-----TRWFED-NGOQTIVTVAEG 135	
Db	63 GKIFGKRLIVDKSSSTAGYMLSTLSLSDSAVYCAAGSSGNKAWDYVGNASVTVSSG 122	
OY	136 KSSGSGSESKPGDVMTPNPLSLPVLGDQASISCRSSQSLHNSGITYLHWYLQKPGQS 195	
Db	123 -SSSGSSSSGSDGVMTQPLSLIPALGQASISCRSSGSLVHNGUTYLNWYLQKAGS 181	
OY	196 PKLLIVYVNRPFSGVPRFSGSGSGDPTFLKLSRVEADLGVYCSQSTHNPYFFGCGTK 255	
Db	182 PKLLIVYVNRPFSGVPRFSGSGSGDPTFLKLSRVEADLGVYCSQSTHNPYFFGCGTK 241	
OY	256 LEIK 259	
Db	242 LEIK 245	
RESULT 11		
ID	AAW53169 standard; Protein; 252 AA.	
XX	AAW53169	
XX	AAW53169;	
DT	16-JUL-1998 (first entry)	
XX		
XX	26-10 anti-digoxin sfv' dimeric construct protein sequence.	
DE		
KW	Antigen imaging; single chain Fv; sfv; linker; dimeric; cancer;	
XX	C-erbB-2; tumour; digoxin; diagnosis.	
OS	Synthetic.	
OS	Mus sp.	
XX		
FH	Key Location/Qualifiers	
FT	Peptide 248..252	
XX	/note="Gly4-Cys C-terminal tail"	
PN	US5753204-A.	
XX		
PD	19-MAY-1998.	
XX		
PF	05-JUN-1995; 95US-0461838.	
XX		
PR	07-OCT-1993; 93US-0133804.	
PR	06-FEB-1992; 92US-0831967.	
PR	05-JUN-1995; 93US-0461838.	

[illegible]

```

XX  US5837846-A.
XX
XX  17-NOV-1998.
XX
XX  05-JUN-1995; 95US-0461386.
XX
XX  07-OCT-1993; 93US-0133804.
XX  06-FEB-1992; 92US-0831967.
XX  05-JUN-1993; 95US-0461386.
XX
XX  (CHIR ) CHIRON CORP.
XX  (CREA-) CREATIVE BIOMOLECULES INC.
XX
XX  Houston LL, Huston JS, Oppermann H, Ring DB;
XX
XX  WPI: 1999-023541/02.
XX  N-PSDB; AAV63398.
XX
XX  Nucleic acid encoding single-chain Fv fragment specific for antigens
XX  - and having C-terminal tail for crosslinking to form dimer with
XX  improved pharmacokinetic properties, used to deliver drugs and
XX  imaging agents, especially to tumours
XX
XX  Example 1; Columns 31-34; 29pp; English.
XX
XX  The present sequence represents an anti-digoxin sfv'. Antibody 26-10
XX  binds digoxin. The present sequence exemplifies the invention.
XX  Dimers of the single chain Fv are used for targeted delivery of
XX  drugs or imaging agents (e.g. cytotoxins, prodrugs or 99m-technetium)
XX  to antigen-expressing cells, particularly for treatment or diagnosis
XX  of tumours (especially of ovary or breast).
XX
XX  Sequence 252 AA:
XX
XX  Query Match 56.7%; Score 927.5; DB 20; Length 252;
XX  Best Local Similarity 76.6%; Pred. No. 1.7e-64;
XX  Matches 187; Conservative 17; Mismatches 33; Indels 7; Gaps 3;
XX
XX  22 VOLOSGAEIVRPGASVTLSCKAGSYFTDYEIHVWQRPVHGLEMIGALDPEGTAVN 81
XX  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX  3 vqlqsgpelvkvpgasvrmcsksgylftdfymwvrqngksldylyispsyvtgyn 62
XX
XX  82 QKFKDAIVTDKSSSTAYMELRSLTSEDSAVYYY----TRWFED-WGQGLVTVSAG 135
XX  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX  63 qkfkqkaltlvdkssstajmeltseedsavyycaqsgsnkwamdyhgasvltvssg 122
XX
XX  136 KSSGSGSRKGDVYVMTPNPLSLPVSLGDDASISCRSSOGLHNSGTYLHMYLQKPGOS 195
XX  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX  123 -sssgsssssgsdvmtcqlpislpvslgddasiscrssgslvhsngnlylnwylqkaqgs 181
XX
XX  186 PRLIYKYNRFGVPPDRFSGSGSGTDFTLKISRVEAEDVGYFCQSTHVPYTFGGGTR 255
XX  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX  182 pkllykysnrfsqvpdrfsgsgsgtdftlkisrveeedlglyfcsqthvptfsggtx 241
XX
XX  256 LEIK 259
XX  |||||
XX  242 leik 245
XX
XX  Db
XX
XX  RESULT 13
XX  AAR27244
XX  ID AAR27244 standard; Protein; 367 AA.
XX
XX  AAR27244;
XX
XX  25-FEB-1993 (first entry)
XX
XX  Sequence encoded by the MLE-mFB-sfv gene in plasmid pH912.
XX
XX  Fusion protein; serine-rich peptide linker; protease resistant.
XX

```

```

OS  Synthetic.
XX
XX  Key Location/Qualifiers
XX  Protein 1..59
XX  FT /label= modified trp LE leader peptide
XX  FT Protein 61..121
XX  FT /label= modified fragment B
XX  FT /note= "Of Staphylococcal protein A"
XX
XX  W09215682-A.
XX
XX  17-SEP-1992.
XX
XX  27-FEB-1992; 92MO-US01478.
XX  27-FEB-1991; 91US-0662226.
XX
XX  (CREA-) CREATIVE BIOMOLECULES INC.
XX
XX  Huston JS, Oppermann H, Timasheff SN;
XX
XX  WPI: 1992-331728/40.
XX  N-PSDB; AAQ28572.
XX
XX  Fusion proteins comprising serine-rich peptide linkers - have
XX  improved solubility in physiological media, resistance to
XX  proteolysis and enhanced regolding properties.
XX
XX  Example; pages 30-32; 49pp; English.
XX
XX  AAR27243 is a pref. linker of the invention. The advantage of such
XX  linkers is that they can improve the refolding properties of the
XX  fusion protein expressed in procarotes. The linker itself is
XX  resistant to proteolysis. In particular it is used to fuse domains
XX  mimicking vh and vl from monoclonal antibody, to produce single
XX  chain binding site proteins (sfv) which dissolve in physiological
XX  media, retain their activity at high concentrations, and resist
XX  lysis by endogenous proteases. pH912 was pred. in order to
XX  evaluate an anti-digoxin 26-10 sfv contg. a Ser-rich peptide
XX  linker.
XX
XX  Sequence 367 AA:
XX
XX  Query Match 66.5%; Score 925.5; DB 13; Length 367;
XX  Best Local Similarity 74.3%; Pred. No. 3.8e-64;
XX  Matches 188; Conservative 19; Mismatches 39; Indels 7; Gaps 3;
XX
XX  13 AAASARAAVOLOSGAEIVRPGASVTLSCKAGSYFTDYEIHVWQRPVHGLEMIGALD 72
XX  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX  115 eqapksdpvqlqsgpelvkvpgasvrmcsksgylftdfymwvrqngksldylyis 174
XX
XX  73 PETGTAIVNOKFKDKAIVTDKSSSTAYMELRSLTSEDSAVYYY----TRWFED-WGQ 126
XX  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX  175 pysvltgynqkfkqkaltlvdkssstajmeltseedsavyycaqsgsnkwamdyhg 234
XX
XX  127 TLVTVAEGKSSGSGSRKGDVYVMTPNPLSLPVSLGDDASISCRSSOGLHNSGTYLH 186
XX  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX  235 asvltvsssg-sssgsssgsdvmtcqlpislpvslgddasiscrssgslvhsngnlyln 293
XX
XX  187 WYLOKPGQSPKRLIYKYNRFGVPPDRFSGSGSGTDFTLKISRVEAEDVGYFCQSTHVP 246
XX  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX  294 wylqkaqspklllykysnrfsqvpdrfsgsgsgtdftlkisrveeedlglyfcsqthv 353
XX
XX  247 PYTFGGGTRLEIK 259
XX  ||||| ||||| |||||
XX  354 ppltfgggtkleik 366
XX
XX  Db
XX
XX  RESULT 14
XX  AAP80154
XX  ID AAP80154 standard; protein; 249 AA.
XX

```

[illegible]

```

Db          246 eik 246

RESULT      15
ID          AAR27245
AC          AAR27245 standard; Protein; 246 AA.
XX
XX          AAR27245.
AC
DT          25-FEB-1993 (first entry)
XX
XX          Sequence of the AA sequences mimicking the light (VL) and
DE heavy (VH) chain variable regions of an antibody linked to jform a
DE single chain antibody binding site (sfv).
XX
XX          Fusion protein; serine-rich peptide linker; protease resistant.
KM
OS          Synthetic.
XX
XX          Key
FT          Location/Qualifiers
FT          Domain                2..120
FT                                /label= VH
FT          Region                121..133
FT                                /label= linker
FT          Domain               134..246
FT                                /label= VL
PN          WO9215682-A.
XX
XX          17-SEP-1992.
PD
XX          27-FEB-1992; 92WO-US01478.
PF
XX          27-FEB-1991; 91US-0662226.
PR
XX          (CREA-) CREATIVE BIOMOLECULES INC.
PA
PI          Huston JS, Oppermann H, Timshaff SN;
XX
DR          WPI; 1992-311728/40.
DR          N-PSDB; AAC28573.
XX
PT          Fusion proteins comprising serine-rich peptide linkers - have
PT improved solubility in physiological media, resistance to
PT proteolysis and enhanced regolding properties.
XX
XX          Example; pages 34-35; 49pp; English.
PS
CC          AAR27243 is a pref'd. linker of the invention. The advantage of such
CC linkers is that they can improve the refolding properties of the
CC fusion protein expressed in procarcytes. The linker itself is
CC resistant to proteolysis. In particular it is used to fuse domains
CC mimicking VH and VI from monoclonal antibody, to produce single
CC chain binding site proteins (sfv) which dissolve in physiological
CC media, retain their activity at high concentrations, and resist
CC lysis by endogenous processes. PH912 was pred. in order to
CC evaluate an anti-digoxin 26-10 sfv contg. a Ser-rich peptide
CC linker.
CC
Sequence    246 AA.
XX
XX
Query Match              66.3%; Score 922.5; DB 13; Length 246;
Best Local Similarity   76.2%; Pred. No. 4e-64;
Matches 186; Conservative 17; Mismatches 34; Indels 7; Gaps 3;
22 VQDQGSCAEIVRPGASVTLSCKRASGYTFTEDEIHWVRQTYPYHGLEWIGALDPETGTAYN 81
||||| :|||:||||| :|||:||||| :|||:||||| :|||:||||| :|||:||||| :
3 vqjhsagpelivkpgasvrmscksgyiftdfyhmwvrgsbgsidsiygyispysgvtlygn 62
82 QREKDAIIVNVKSSSTAYMELRLSTSDDSAVVYY-----TRFED-WGGGLIYTVYSAG 135
63 qktfgrkatltvdssstaymelrltsdsavvyccagsngkwamdywgvgasvatvsssg 122

```

```
QY 136 KSSGSGSESKPGDVVMTPNPLSLPVSLGDOASISCRSSOSLHSGITVLMWYLOKPGOS 195
Db 123 -sssgsssgsdvymtqdpLslpvsLgddasiscrsqslvhsngntylmwyLqkaqs 181
QY 196 PKLLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEAEDIGVFCQSSTHVPYTFGGGTR 255
Db 182 PKLLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEAEDIGVFCQSSTHVPYTFGGGTR 241
QY 256 LEIK 259
Db 242 LEIK 245
```

Search completed: January 18, 2002, 01:23:47
Job time: 2620 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 18, 2002, 00:41:18 ; Search time 26.93 seconds
(without alignments)
224.782 Million cell updates/sec

Title: US-09-358-321C-32
1391

Perfect score: 1 MVSALVLYVLLAAAHSAFA.....FGGOTKLEIKERKLISEEDL 269

Sequence: BLOCUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued Patents AA:*
2: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
3: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	928.5	66.8	367	1 US-08-257-341-5	Sequence 5, Appl
2	927.5	66.7	246	1 US-08-257-341-7	Sequence 7, Appl
3	927.5	66.7	252	1 US-08-133-804-4	Sequence 4, Appl
4	927.5	66.7	252	1 US-08-461-838-4	Sequence 4, Appl
5	927.5	66.7	252	1 US-08-461-838-4	Sequence 4, Appl
6	848.5	61.0	260	2 US-09-070-408-132	Sequence 132, App
7	818.5	58.8	260	2 US-08-447-402-1	Sequence 1, Appl
8	808.5	58.0	247	4 US-09-227-693-34	Sequence 34, Appl
9	806.5	58.0	248	1 US-08-331-398A-34	Sequence 34, Appl
10	806.5	58.0	248	2 US-08-331-398B-34	Sequence 34, Appl
11	806.5	58.0	248	2 US-08-759-804A-34	Sequence 34, Appl
12	788.5	56.7	638	4 US-09-070-637-20	Sequence 20, Appl
13	767	55.1	273	2 US-08-403-853-18	Sequence 18, Appl
14	762	54.8	365	3 US-08-875-811-53	Sequence 53, Appl
15	762	54.8	365	3 US-08-875-811-53	Sequence 53, Appl
16	761.5	54.7	281	4 US-09-025-769B-178	Sequence 178, App
17	761	54.7	271	2 US-08-894-922A-10	Sequence 10, Appl
18	755.5	54.3	252	2 US-08-752-844-66	Sequence 66, Appl
19	747	53.7	262	2 US-08-894-922A-14	Sequence 14, Appl
20	742	53.3	235	3 US-08-279-772A-8	Sequence 8, Appl
21	742	53.3	235	3 US-08-279-772A-8	Sequence 8, Appl
22	741	53.3	553	4 US-08-902-486-11	Sequence 11, Appl
23	740.5	53.2	483	2 US-08-392-338A-19	Sequence 19, Appl
24	740.5	53.2	483	2 US-09-166-750-19	Sequence 19, Appl
25	740.5	53.2	483	3 US-09-166-093-19	Sequence 19, Appl
26	740.5	53.2	483	3 US-09-172-019-19	Sequence 19, Appl
27	740.5	53.2	483	3 US-09-166-094-19	Sequence 19, Appl

ALIGNMENTS

28	740	53.2	553	2 US-08-263-911-9	Sequence 9, Appl
29	739	53.1	289	3 US-09-184-658-63	Sequence 63, Appl
30	739	53.1	599	1 US-08-463-163-3	Sequence 3, Appl
31	728.5	52.4	244	2 US-08-553-497A-20	Sequence 20, Appl
32	726.5	52.2	246	2 US-08-553-497A-24	Sequence 24, Appl
33	718	51.6	246	1 US-08-469-486-57	Sequence 57, Appl
34	718	51.6	246	1 US-08-469-486-57	Sequence 57, Appl
35	713.5	51.3	244	2 US-08-553-497A-22	Sequence 22, Appl
36	709.5	51.0	242	2 US-08-553-497A-26	Sequence 26, Appl
37	705	50.7	282	2 US-08-860-174A-10	Sequence 10, Appl
38	698.5	50.2	242	2 US-08-553-497A-28	Sequence 28, Appl
39	696.5	50.1	637	1 US-08-233-838-16	Sequence 16, Appl
40	696.5	50.1	637	2 US-08-465-473B-16	Sequence 16, Appl
41	693	49.8	553	2 US-08-661-052-16	Sequence 16, Appl
42	693	49.8	553	4 US-09-188-082-16	Sequence 16, Appl
43	689	49.5	240	2 US-08-800-198-8	Sequence 8, Appl
44	689	49.5	240	3 US-09-296-595-8	Sequence 8, Appl
45	688	49.5	270	2 US-08-652-507-2	Sequence 2, Appl

RESULT 1
US-08-257-341-5
Sequence 5, Application US/08257341
Patent No. 5525491
GENERAL INFORMATION:
APPLICANT: HUSTON, JAMES S
APPLICANT: OPPERMAN, HERMANN
APPLICANT: TIMASHEFF, SERGE N
TITLE OF INVENTION: SERINE RICH PEPTIDE LINKER
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
STREET: 35 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,341
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/842,149
FILING DATE:
APPLICATION NUMBER: US 07/662,226
FILING DATE: 27-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, ESQ, PAULA A
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: CRP-064CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000 (ATTY)
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 367 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-257-341-5
Query Match 66.8%; Score 928.5; DB 1; Length 367;
Best Local Similarity 74.7%; Pred. No. 7.7e-80;
Matches 189; Conservative 18; Mismatches 39; Indels 7; Gaps 3;

DB 63 QKFKGKATLVDPKSSSTAYMELRSLTSEDASVYVCAGSSGKMKAMDYWGCHASVTYSSG 122
QY 136 KSSGSGSESKPDVYMTPTPLSLPVSLDQASISCRSSQSLHNSNGITTYLHWYLQKPGQS 195
DB 123 -SSSSGSSSGSDVYMTPTPLSLPVSLDQASISCRSSQSLHNSNGITTYLHWYLQKPGQS 181
QY 196 PRLIYKYSNRFSGVDPDRFSSGSGTDTTLKISRVEADLGLGVYFCSSQSTHVPYTFGGGTR 255
DB 182 PRLIYKYSNRFSGVDPDRFSSGSGTDTTLKISRVEADLGLGVYFCSSQSTHVPYTFGGGTR 241
QY 256 LEIK 259
DB 242 LEIK 245

RESULT 4
US-08-461-838-4
Sequence 4, Application US/08461838
Patent No. 5753204
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461.838
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-838-4

Query Match 66.7%; Score 927.5; DB 1; Length 252;
Best Local Similarity 76.6%; Pred. No. 5.7e-80;
Matches 187; Conservative 17; Mismatches 33; Indels 7; Gaps 3;
QY 22 VOLQSGAELVPRGASVTLSCASGYTTDEIHWVROTPVHGLEMTGALDPEGTATYN 81
DB 3 VOLQSGPELVKPGASVMSCKSSGYITFDYMMNVQSHGKSLDIYGISPYSGVTGYN 62
QY 82 QKFKDAIYVDKSSSTAYMELRSLTSEDASVYVY----TRWED--WGGLTVYSAEG 135
DB 63 QKFKGKATLVDPKSSSTAYMELRSLTSEDASVYVCAGSSGKMKAMDYWGCHASVTYSSG 122
QY 136 KSSGSGSESKPDVYMTPTPLSLPVSLDQASISCRSSQSLHNSNGITTYLHWYLQKPGQS 195

DB 123 -SSSSGSSSGSDVYMTPTPLSLPVSLDQASISCRSSQSLHNSNGITTYLHWYLQKPGQS 181
QY 196 PRLIYKYSNRFSGVDPDRFSSGSGTDTTLKISRVEADLGLGVYFCSSQSTHVPYTFGGGTR 255
DB 182 PRLIYKYSNRFSGVDPDRFSSGSGTDTTLKISRVEADLGLGVYFCSSQSTHVPYTFGGGTR 241
QY 256 LEIK 259
DB 242 LEIK 245

RESULT 5
US-08-461-386-4
Sequence 4, Application US/08461386
Patent No. 5837846
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461.386
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-386-4

Query Match 66.7%; Score 927.5; DB 2; Length 252;
Best Local Similarity 76.6%; Pred. No. 5.7e-80;
Matches 187; Conservative 17; Mismatches 33; Indels 7; Gaps 3;
QY 22 VOLQSGAELVPRGASVTLSCASGYTTDEIHWVROTPVHGLEMTGALDPEGTATYN 81
DB 3 VOLQSGPELVKPGASVMSCKSSGYITFDYMMNVQSHGKSLDIYGISPYSGVTGYN 62
QY 82 QKFKDAIYVDKSSSTAYMELRSLTSEDASVYVY----TRWED--WGGLTVYSAEG 135
DB 63 QKFKGKATLVDPKSSSTAYMELRSLTSEDASVYVCAGSSGKMKAMDYWGCHASVTYSSG 122
QY 136 KSSGSGSESKPDVYMTPTPLSLPVSLDQASISCRSSQSLHNSNGITTYLHWYLQKPGQS 195
DB 123 -SSSSGSSSGSDVYMTPTPLSLPVSLDQASISCRSSQSLHNSNGITTYLHWYLQKPGQS 181
QY 196 PRLIYKYSNRFSGVDPDRFSSGSGTDTTLKISRVEADLGLGVYFCSSQSTHVPYTFGGGTR 255

Db 182 PKLIIVYVSNRFGSVDRFGSGSDFTLKISRVKAEADLGITYFCSQTHVPTFGGK 241
QY 256 LEIK 259
Db 242 LEIK 245

RESULT 6

US-09-070-408-132
; Sequence 132, Application US/09070408
; Patent No. 6180341
; GENERAL INFORMATION:
; APPLICANT: Iverson, Brent L.
; APPLICANT: Butts, Elizabeth A.
; TITLE OF INVENTION: IN VITRO SCANNING SATURATION MUTAGENESIS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,408
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/045,409
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: McMillan, Nabeeja R.
; REGISTRATION NUMBER: P-43,363
; REFERENCE/DOCKET NUMBER: UTSS:593
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/447-7577
; INFORMATION FOR SEQ ID NO: 132:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-070-408-132

Query Match 61.0%; Score 848.5; DB 4; Length 269;
Best Local Similarity 69.7%; Pred. No. 1.8e-72;
Matches 170; Conservative 23; Mismatches 44; Indels 7; Gaps 3;

QY 22 VOLQSGAEIVRPGASVTLSCKASGYFTDYELHWVRQTPVHGLEWIGALIDPETGTAAYN 81
Db 3 VOLQSGPELVKPGASVYMSCKSSGYFTDFYMWVRQSHGKSLDYIGTISPSGYTGIN 62
QY 82 QKFKKATLVYDKSSSTAYMELRSLTSEDSAVYYY-----TRWFED-WGQGLVTVSAEG 135
Db 63 QKFKKATLVYDKSSSTAYMELRSLTSEDSAVYYYCASSGNKWMYWGASVTVSSG 122
QY 136 KSSGSGSESRPG-DVYMTNPPLSPVSLGQASISCRSSQSLHNSGITYLHWYLOKPG 194
Db 123 GSGSGGGGGSDIVLTQTPPLSPVSLGQATISCRSSQSLHNSGNTYLMWYLOKAG 182
QY 195 SKLLIIVYVSNRFGSVDRFGSGSDFTLKISRVAEDLGITYFCSQTHVPTFGGK 254
Db 183 SKLLIIVYVSNRFGSVDRFGSGSDFTLTIDRVEDDAIYCSQTHVPTFGSGT 242

QY 255 KLEI 258
Db 243 KLEI 246

RESULT 7

US-08-447-402-1
; Sequence 1, Application US/08447402
; Patent No. 586344
; GENERAL INFORMATION:
; APPLICANT: Iverson, Brent
; APPLICANT: Georgiou, George
; TITLE OF INVENTION: IMMUNOASSAY AND ANTIBODY SELECTION
; TITLE OF INVENTION: METHODS USING CELL SURFACE EXPRESSED
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,402
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/258,543
; FILING DATE: 10-JUN-1994
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/794,731
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSS:584KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 260 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-447-402-1

Query Match 58.8%; Score 818.5; DB 2; Length 260;
Best Local Similarity 66.9%; Pred. No. 1.2e-69;
Matches 164; Conservative 26; Mismatches 48; Indels 7; Gaps 3;

QY 22 VOLQSGAEIVRPGASVTLSCKASGYFTDYELHWVRQTPVHGLEWIGALIDPETGTAAYN 81
Db 2 VOLQSGPELVKPGASVYMSCKSSGYFTDFYMWVRQSHGKSLDYIGTISPSGYTGIN 61
QY 82 QKFKKATLVYDKSSSTAYMELRSLTSEDSAVYYY-----TRWFED-WGQGLVTVSAEG 135
Db 62 QKFKKATLVYDKSSSTAYMELRSLTSEDSAVYYYCASSGNKWMYWGASVTVSSG 121
QY 136 KSSGSGSESRPG-DVYMTNPPLSPVSLGQASISCRSSQSLHNSGITYLHWYLOKPG 194
Db 122 GSGSGGGGGSDIVLTQTPPLSPVSLGQATISCRSSQSLHNSGNTYLMWYLOKPG 181

OY 22 VQLDGGAEILVRGASVLTSCAGSYPTFDIEHWRCQPVHGKLEWIGAIIDPETGTAYN 81
 | :
Db 3 VKLVESGGGLVQPGSGSLKLSCTSGFTISDYIMRWNQTEERKLEWVAIISNDSSAYS 62
 | :

Best Local Similarity 63.7%; Pred. No. 1,5e-68;
Matches 156; Conservative 29; Mismatches 53; Indels 7; Gaps 2;

```

QY 22 VQLQSGAEIVRPGASVTLSCKASGYTFDYEIHVWROTVPVHGLEIGNAIDPETGTAYN 81
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3 VKLVESGGHIVPGSGIKLSCATSGFTFSDYKMWVWQRPKRELEWAVASINDSSAAYS 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 82 QKFKDAIVTVDKSSSTAYMELSLTSEDAVYYTR-----WFDWQGLTVYSAG 135
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63 DTVVGRFTTISRDNAKRNLYLQMSRLKSEDTAISCARGLAMGFYWGQGLTVYSSGG 122
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 136 KSSGSGSESKPG-DVYVTPMLPLPVSLGQASISCRSSQSLHNSGITYLHMYLQKPG 194
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 123 GSGSGGSGGGGSDVLTMTQSLPLPVSLGQASISCRSSQSLHNSGITYLHMYLQKPG 182
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 195 SPKLLIKVSNRSGVDNRSGSGGDTFLTKISRVKADLGVYFCOSTHVPYFGGCT 254
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 183 SPKLLIKVSNRSGVDPDRSGSGGDTFLTKISRVKADLGVYFCOSTHVPYFGGCT 242
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 255 KLEIK 259
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 243 KLEIK 247
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 12
US-09-070-637-20
: Sequence 20, Application US/09070637A
: Patent No. 6133722
: GENERAL INFORMATION:
: APPLICANT: SIMERS, NATHAN O.
: APPLICANT: YARNOLD, SUSAN
: APPLICANT: SENTER, PETER D.
: TITLE OF INVENTION: RECOMBINANT ANTIBODY-ENZYM FUSION PROTEINS
: FILE REFERENCE: 9197F-83-1
: CURRENT APPLICATION NUMBER: US/09/070,637A
: EARLIER FILING DATE: 1998-04-30
: EARLIER APPLICATION NUMBER: 60/045,888
: EARLIER FILING DATE: 1997-05-07
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: Patentin Ver. 2.0
: SEQ ID NO 20
: LENGTH: 638
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Amino acid
: OTHER INFORMATION: sequence for L49-sfv-bl including Pals leader
US-09-070-637-20

```

Query Match 56.7%; Score 788.5; DB 4; Length 638;
Best Local Similarity 60.4%; Pred. No. 2.7e-66;
Matches 165; Conservative 31; Mismatches 60; Indels 17; Gaps 5;

```

QY 10 LLAASASAPAAVLOOQSGAEIVRPGASVTLSCKASGYTFDYEIHVWROTVPVHGLEWIC 69
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 12 LLLLAAPAAAEVLOQSGPSLVKPSOTLSLTCSVTGDSITSGYMWIKPFGNKLEYWG 71
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 70 AIDETGGTAVYNOKFKDAIVTVDKSSSTAYMELSLTSEDAVY-----YTRWF 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 72 YIS-DSGITVYNPILSKRISITRDTSKNYLQNLNFYADATATYCARPLATYYA--M 128
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 EDWQGLTVYSAGKSS-----GSGSRSKPGDVYVMTNPPLSLPVSLGQASISCRSSQSL 176
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 129 DYWGQGLTVYSSGSGTSGSKPSSGEGSLTGDVMTQPLSLPVSLGQASISCRASQSL 188
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 177 LHSNGITYLHMYLQKPGSPKLLIYKSNRFGSVDPDRSGSGGDTFLTKISRVKADLGV 236
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 189 VHSNGNTLHMYLQKPGSPKLLIYKSNRFGSVDPDRSGSGGDTFLTKISRVKADLGV 248
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 237 VYFCOSTHVPYFGGCTKLEIKLEIKLEIKLEIKLEIKLEIKLEIKLEIKLEIKLEIK 269
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 249 VYFCOSTHVPYFGGCTKLEIKRTP-VSEKOL 280
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 13
US-08-403-853-18
: Sequence 18, Application US/08403853
: Patent No. 5844094
: GENERAL INFORMATION:

```

: APPLICANT: HUDSON, Peter J.
: APPLICANT: LAH, Maria
: APPLICANT: KORRT, Alex A.
: APPLICANT: IRVING, Robert A.
: APPLICANT: ALWELL, John L.
: APPLICANT: MALBY, Robyn L.
: APPLICANT: POWER, Barbara E.
: APPLICANT: COLMAN, Peter M.
: TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
: NUMBER OF SEQUENCES: 25
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Foley & Lardner
: STREET: 3000 K Street, N.W., Suite 500
: City: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20007-5109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/403,853
: FILING DATE: 30-MAY-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/AU93/00491
: FILING DATE: 24-SEP-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: AU PL 4973
: FILING DATE: 25-SEP-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: BENT, Stephen A.
: REGISTRATION NUMBER: 29,768
: REFERENCE/DOCKET NUMBER: 16786/189/CHAC
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)672-5300
: TELEFAX: (202)672-5399
: TELEX: 904136
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 273 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-403-853-18

```

Query Match 55.1%; Score 767; DB 2; Length 273;
Best Local Similarity 59.5%; Pred. No. 9.1e-65;
Matches 156; Conservative 28; Mismatches 64; Indels 14; Gaps 3;

```

QY 10 LLAASASAPAAVLOOQSGAEIVRPGASVTLSCKASGYTFDYEIHVWROTVPVHGLEWIC 69
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 12 LLLLAAPAAAOVLOOQSGAEIVKPGASVMSKASGYFTTNNMWKQSGGGLIEWIC 71
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 70 AIDETGGTAVYNOKFKDAIVTVDKSSSTAYMELSLTSEDAVY-----YTRWF 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 72 IFYNGDGTAVNOKFKDAITLADKSSNTAYMQLSLTSEDAVYVCARSGSYRVDG 131
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 EDWQGLTVYSAGKSSGSGSKPGDVYVMTNPPLSLPVSLGQASISCRSSQSLHNS 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 132 DYWGQGLTVYSSGSGGSGSGGSDIELTQTSSLSASLGDRTYISCRASODI--SN 189
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 GITYLHMYLQKPGSPKLLIYKSNRFGSVDPDRSGSGGDTFLTKISRVKADLGVYFC 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 190 ---LYNMVQNPQSTVLLIYYTSNLSHSEVPSRFSSGSGSTDTSLTISNLEQEDTATYRC 246
QY 241 SQSTHVPYRTGGGTKEIKEEK 262
Db 247 QODETLPTFTGGGTKEIKRIDYK 268

RESULT 14

US-08-875-811-53
Sequence 53, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluís
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-53

Query Match 54.8%; Score 762; DB 3; Length 365;

Best Local Similarity 59.9%; Pred. No. 4e-64; Indels 4; Gaps 2;

Matches 145; Conservative 43; Mismatches 50; Indels 4; Gaps 2;

QY 22 VOLOQSGAEIVRGASVYTLSCKASGYTFDTYELHWVROTVPVHGLEWIGAIDPETGCTAYN 81
Db 120 VKLOQSGPELKKPGETVYKISCKASGYTFDTYGNMVKQAPGKGLKMGMINITYGESIYA 179
QY 82 QKFRDAIVTVDKSSSTAYMELSLTSEDSAVYYTRWF--EDWGQGLTVYSAEGKSS 138
Db 180 DDEGRFAFLSTETSAASAAYLQINNLEKNEEDATYFCARFAIKGQYWGQGTIVTVSSGGGGS 239
QY 139 GSGSESKPG--DYVMTNPPLSLPVSLGDOASISCRSSQSLHNSNGITYLHWYLOKPGQSPK 197
Db 240 GGGGSGGGSDIVLTQSPFSPNPTLTGTSASISCRSTKSLHNSNGITYLHWYLOKPGQSPQ 299

QY 198 LLIYVNSRRSGVDRFSSGSGSTDTFLKISRVEADLQVYRCQSTHVPYRTGGGTKE 257
Db 300 LLIIQMSNLASGVDRFSSGSGSTDTFLRISRVEADVGVYCAQNLPTFTGGGTKE 359
QY 258 IK 259
Db 360 IK 361

RESULT 15

US-08-875-811-55
Sequence 55, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluís
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-55

Query Match 54.8%; Score 762; DB 3; Length 366;

Best Local Similarity 59.9%; Pred. No. 4e-64; Indels 4; Gaps 2;

Matches 145; Conservative 43; Mismatches 50; Indels 4; Gaps 2;

QY 22 VOLOQSGAEIVRGASVYTLSCKASGYTFDTYELHWVROTVPVHGLEWIGAIDPETGCTAYN 81
Db 3 VKLOQSGPELKKPGETVYKISCKASGYTFDTYGNMVKQAPGKGLKMGMINITYGESIYA 62
QY 82 QKFRDAIVTVDKSSSTAYMELSLTSEDSAVYYTRWF--EDWGQGLTVYSAEGKSS 138
Db 63 DDEGRFAFLSTETSAASAAYLQINNLEKNEEDATYFCARFAIKGQYWGQGTIVTVSSGGGGS 122
QY 139 GSGSESKPG--DYVMTNPPLSLPVSLGDOASISCRSSQSLHNSNGITYLHWYLOKPGQSPK 197
Db 123 GGGGSGGGSDIVLTQSPFSPNPTLTGTSASISCRSTKSLHNSNGITYLHWYLOKPGQSPQ 182

Oy 198 LLITKVSNRFGVPPDRFSGSGGTDTFTLKISRVEAEDDGVYFCSQSTHVPYTFGGGTKLE 257
Db 193 LLITOMSNLASGVPPDRFSSGSGTDTFTLRISRVEAEDVGYCAONLEIPRTFGGGTKLE 242
Oy 258 IK 259
Db 243 IK 244

Search completed: January 18, 2002, 01:24:42
Job time: 2604 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 18, 2002, 00:43:38 ; Search time 37.19 Seconds

(Without alignments)
550.980 Million cell updates/sec

Title: US-09-358-321c-32

Perfect score: 1391
Sequence: 1 MVSALVLYVLAHAHAFA.....FGGKTLEKEKLESEEDL 269

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	748.5	53.8	249	2 S41374	single chain Fv an
2	662.5	47.6	268	2 A56446	Ig heavy chain V r
3	636.5	45.8	233	2 JCS522	p53 specific singl
4	563	40.5	112	2 E27887	Ig kappa chain V r
5	562	40.4	112	2 S32189	Ig kappa chain V r
6	558	40.1	118	2 PT0359	Ig kappa chain V r
7	558	40.1	131	2 B34904	Ig kappa chain pre
8	554	39.8	112	2 D27887	Ig kappa chain V r
9	554	39.8	112	2 S53750	antibody Fab Jel 1
10	554	39.8	115	2 S60066	Ig kappa chain V r
11	554	39.8	131	2 B32513	Ig kappa chain pre
12	554	39.8	131	2 C34904	Ig kappa chain pre
13	552	39.7	111	2 PL0257	Ig kappa chain V r
14	552	39.7	112	2 A27887	Ig kappa chain V r
15	551	39.6	115	2 S38715	Ig kappa chain V r
16	551	39.6	131	2 B30577	Ig kappa chain pre
17	549	39.5	112	2 B27887	Ig kappa chain pre
18	547	39.3	112	2 B31485	Ig kappa chain V r
19	547	39.3	113	2 B41940	Ig kappa chain V r
20	546	39.3	112	2 C27887	Ig kappa chain V r
21	544	39.1	112	2 G34903	Ig kappa chain pre
22	541	39.0	131	2 D34904	Ig kappa chain pre
23	538	38.9	112	2 A49715	Ig kappa chain V r
24	538	38.7	131	2 PT0178	Ig kappa chain pre
25	537	38.6	131	2 D29380	Ig kappa chain pre
26	534	38.4	113	1 KWS26	Ig kappa chain pre
27	534	38.4	113	1 KWS26	Ig kappa chain V r
28	534	38.4	132	2 PH0205	anti-DNA autoantib
29	534	38.4	219	2 S16112	Ig kappa chain V r

30	531	38.2	131	2 S52449	Ig kappa chain V r
31	529	38.0	112	2 A31807	Ig kappa chain V r
32	527	37.9	131	2 B39276	Ig kappa chain pre
33	526	37.8	107	2 D32530	Ig kappa chain V r
34	524	37.7	110	2 S26335	Ig kappa chain V r
35	523	37.6	113	2 PL0203	Ig kappa chain V r
36	522	37.5	217	2 S42772	anti-DNA autoantib
37	522	37.5	219	2 S52028	Ig kappa chain - m
38	521	37.5	219	2 PC4203	Ig kappa chain (mo
39	520	37.4	219	2 S38865	Ig kappa chain - m
40	519.5	37.3	130	2 C29380	Ig kappa chain pre
41	519	37.3	112	2 F27887	Ig kappa chain V r
42	513	36.9	112	2 S38719	Ig kappa chain V r
43	512	36.8	103	2 PH1030	Ig light chain V r
44	512	36.8	108	2 E35350	Ig light chain V r
45	510	36.7	114	2 A32967	Ig kappa chain V-I

ALIGNMENTS

```
RESULT 1
S41374
single chain Fv antibody - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: S41374
R:Artsenko, O.; Weiler, E.W.; Kuentz, K.; Conrad, U.
Submitted to the EMBL Data Library, January 1994
A:Description: Construction and functional characterization of a single chain Fv ant
A:Reference number: S41374
A:Accession: S41374
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <ART>
A:Cross-references: EMBL:229480

Query Match          53.8%; Score 748.5; DB 2; Length 249;
Best Local Similarity 61.1%; Pred. No. 1,4e+48;
Matches 151; Conservative 29; Mismatches 56; Indels 11; Gaps 3;

QY 22 VOLQSGAELVREPASVLTSCRASGYTFDYEIFHWYQTPVHGLEMIGALDPETGGTAYN 81
D 2 VOLQSGAELVREPASVLTSCRASGYTFDYEIFHWYQTPVHGLEMIGALDPETGGTAYN 61
QY 82 QKFDKALIVYDKSSSTAYWELSLTSEDSAYVYTRMFD-----WGQGLVYVSA 133
D 62 PRFDKRTITADTSSNAYLLSLTSEDTAVYCAR--RDTLYTSLGTYWGQSTVIVS 119
QY 134 EGKSSGSGSESRKG-DVWMTPNPLSLVSLGDOASISCRSSQSLHSNGITYLHWYLOKP 192
D 120 RGGSSGSGSGSGGSDIELHQSPSPVYVIGESVTSICSSKSLXYSDODSYLFWFLQRP 179
QY 193 GQSPKLLIYVSNRFSVPVPRFSGSGGDTFLIKISRYVAEDLGYFSGQSHVYTTGG 252
D 180 GQSPKLLIYVSNRFSVPVPRFSGSGGDTFLIKISRYVAEDLGYFSGQSHVYTTGG 239
QY 253 GTRKLEIK 259
D 240 GTRKLEIK 246

RESULT 2
A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C:Species: Mus musculus (house mouse)
C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C:Accession: A56446
R:Tang, P.M.; Folitz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally ic
A:Reference number: A56446; M13:95229583
```


A:Reference number: PT0352; MUID:91108325
A:Accession: P0359
A:Molecule type: mRNA
A:Residues: 1-118 <SH>
A:Experimental source: strain BALB/c
C:Comment: This protein is an anti-double-stranded DNA antibody.
C:Superfamily: immunoglobulin V region; immunoglobulin homology F:19-98/Domain: immunoglobulin homology <IMM>

Query Match 40.1%; Score 558; DB 2; Length 118;
Best Local Similarity 95.5%; Pred. No. 8e-35;
Matches 107; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 148 DVMVTNPFLSLPVSIAGDQASISCRSSQSILHSNGITVTHWYLQRKQGSPKLTIKYVSNR 207
 ||||| |
DB 4 DVMVTGTPLSLPLVSGDDASISCRSSQSLVHNSGTIVTHWLQKRQGSFKLLTIKYVSNR 63

OY 208 SGVPDRFGSGSGLDTFTLKISRVEADLGVFYCSTHVPTFFGGTKLEIK 259
 ||||| |
DB 64 SGVPDRFGSGSGLDTFTLKISRVEADLGVFYCSTHVPTFFGGTKLEIK 115

RESULT 7
 B34904
I9 kappa chain precursor V region (12-40 and 5-14) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000
C:Accession: B34904; H34903
J:Reedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J: Biol. Chem. 265, 133-138, 1990
A>Title: Active site structure and antigen binding properties of idiotypically cross-reactive monoclonal antibodies
A:Reference number: A34903; MUID:90094387
A:Accession: B34904
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-131 <BED>
A:CROSS-references: GB:M2384; GB:J05237; GB:J05238; NID:9639656; PIDN:AA61589.1; PID:gag
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 40.1%; Score 558; DB 2; Length 131;
Best Local Similarity 95.5%; Pred. No. 9.1e-35;
Matches 107; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 148 DVMVTNPFLSLPVSIAGDQASISCRSSQSILHSNGITVTHWYLQRKQGSPKLTIKYVSNR 207
 ||||| |
DB 20 DVMVTGTPLSLPLVSGDDASISCRSSQSLVHNSGTIVTHWLQKRQGSFKLLTIKYVSNR 79

OY 208 SGVPDRFGSGSGLDTFTLKISRVEADLGVFYCSTHVPTFFGGTKLEIK 259
 ||||| |
DB 80 SGVPDRFGSGSGLDTFTLKISRVEADLGVFYCSTHVPTFFGGTKLEIK 131

RESULT 8
 D27887
I9 kappa chain V region (H35-2) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C:Accession: D27887
R:Catton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A>Title: Structural and functional implications of a restricted antibody response to a conserved epitope of the major histocompatibility complex class II molecule I-E_d
A:Reference number: A91043; MUID:86300658
A:Accession: D27887
A:Molecule type: DNA
A:Residues: 1-112 <CAR>
A:Experimental source: strain Balb/c
A>Note: This sequence was determined from the germ-line gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus hemagglutinin
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin F;16-95/Domain: Immunoglobulin homology <IMM>

Query Match 39.8%; Score 554; DB 2; Length 112;
Best Local Similarity 94.6%; Pred. No. 1,5e-34;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 148 DVMATPNPLSPVSLGQASISCRSSQSLHNSGITYLHMYLQKPPQSKLLIKYSNRF 207
|||||
D 1 DVMATQPLSLPVSLGQASISCRSSQSLHNSGNTLYLHMYLQKPPQSKLLIFKYSNRF 60
|||||

QY 208 SGVDFRFGSSGSDFTLKISRVAEDLGVPFCSQSTHVPYTFGGGTKEIK 259
|||||
D 61 SGVDFRFGSSGSDFTLKISRVAEDLGVPFCSQSTHVPYTFGGGTKEIK 112
|||||

RESULT 9
553750
antibody Fab Jcl 103 light chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000
C:Accession: S53750
R:Pokkikulr, P.R.; Bouthillier, F.; Li, Y.; Kuderova, A.; Lee, J.; Cygler, M.
J. Mol. Biol. 243, 283-297, 1994
A:Title: Preparation, characterization and crystallization of an antibody Fab
A:Reference number: S53750; MUID:95018269
A:Accession: S53750
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <POK>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 39.8%; Score 554; DB 2; Length 112;
Best Local Similarity 95.5%; Pred. No. 1,5e-34;
Matches 107; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 148 DVMATPNPLSPVSLGQASISCRSSQSLHNSGITYLHMYLQKPPQSKLLIKYSNRF 207
|||||
D 1 DVMATQPLSLPVSLGQASISCRSSQSLHNSGNTLYLHMYLQKPPQSKLLIFKYSNRF 60
|||||

QY 208 SGVDFRFGSSGSDFTLKISRVAEDLGVPFCSQSTHVPYTFGGGTKEIK 259
|||||
D 61 SGVDFRFGSSGSDFTLKISRVAEDLGVPFCSQSTHVPYTFGGGTKEIK 112
|||||

RESULT 10
S60066
Ig kappa chain V region (monoclonal antibody C3) [validated] - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Feb-1996 #sequence_revision 10-Oct-1997 #text_change 23-Mar-2001
C:Accession: S60066
R:Wien, M.W.; Filman, D.J.; Stura, E.A.; Guillot, S.; Delpeyroux, F.; Crainic, R.;
Mat. Struct. Biol. 2, 232-243, 1995
A:Title: Structure of the complex between the Fab F16-95 of a neutralizing antio
A:Reference number: S60066; MUID:95292109
A:Accession: S60066
A:Molecule type: mRNA
A:Residues: 1-115 <WIE>
A:Cross-references: EMBL:X84697; NID:g773226
R:Wien, M.W.; Hogle, J.M.
submitted to the Brookhaven Protein Data Bank, January 1995
A:Reference number: A52979; PDB:1FPT
A:Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 1-23,'S',25
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>
F:23-93/Disulfide bonds: #status experimental

Query Match 39.8%; Score 554; DB 2; Length 115;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 18, 2002, 01:24:48 ; Search time 26.45 Seconds

(without alignments)
372.886 Million cell updates/sec

Title: US-09-358-321c-32

Perfect score: 1391

Sequence: 1 MWSAIVLYVLLAAAHSAFA.....FGGCTKLEKEKLISEBDL 269

Scoring table: BLOSUM62

Gapcp 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	534	38.4	113	1	KV2G_MOUSE
2	460	33.1	113	1	KV2F_HUMAN
3	457	32.9	113	1	KV2D_HUMAN
4	454	32.6	113	1	KV2E_MOUSE
5	454	32.6	117	1	KV2E_HUMAN
6	445.5	32.0	119	1	HV07_MOUSE
7	436	31.3	112	1	KV2D_MOUSE
8	435	31.3	113	1	KV2B_HUMAN
9	431.5	31.0	115	1	KV2A_HUMAN
10	431.5	31.0	137	1	HV11_MOUSE
11	423	30.4	138	1	HV48_MOUSE
12	420	30.2	113	1	KV2F_MOUSE
13	417.5	30.0	112	1	KV2C_HUMAN
14	411	29.5	117	1	HV12_MOUSE
15	411	29.5	117	1	HV13_MOUSE
16	409	29.4	117	1	HV49_MOUSE
17	407.5	29.3	118	1	HV51_MOUSE
18	405.5	29.2	120	1	HV50_MOUSE
19	405	29.1	117	1	HV09_MOUSE
20	403	29.0	120	1	HV03_MOUSE
21	400	28.8	140	1	HV02_MOUSE
22	393	28.3	136	1	HV15_MOUSE
23	392	28.2	117	1	HV10_MOUSE
24	391	28.1	117	1	HV04_MOUSE
25	388	27.9	113	1	KV2C_MOUSE
26	383.5	27.6	134	1	KV4C_HUMAN
27	383	27.5	133	1	KV4B_HUMAN
28	382.5	27.5	114	1	KV4A_HUMAN
29	381	27.4	112	1	KV2A_MOUSE
30	381	27.4	117	1	HV05_MOUSE
31	381	27.4	117	1	HV14_MOUSE
32	380	27.3	117	1	HV06_MOUSE
33	376.5	27.1	108	1	KV1_CANFA

34	376.5	27.1	111	1	KV3H_MOUSE	P01660 mus musculu
35	371.5	26.7	111	1	KV3C_MOUSE	P01656 mus musculu
36	371.5	26.7	111	1	KV3L_MOUSE	P01664 mus musculu
37	370.5	26.6	111	1	KV3R_MOUSE	P01670 mus musculu
38	370	26.6	121	1	HV01_MOUSE	P01745 mus musculu
39	368.5	26.5	111	1	KV3A_MOUSE	P01654 mus musculu
40	365.5	26.3	111	1	KV3D_MOUSE	P03977 mus musculu
41	363.5	26.1	111	1	KV3E_MOUSE	P01671 mus musculu
42	363.5	26.1	131	1	KV3I_MOUSE	P01671 mus musculu
43	363	26.1	112	1	KV3B_MOUSE	P01655 mus musculu
44	362.5	26.1	111	1	KV3J_MOUSE	P01652 mus musculu
45	362.5	26.1	111	1	KV3T_MOUSE	P01672 mus musculu

ALIGNMENTS

RESULT	ID	QUERY	STANDARD	PRT	113 AA
KV2G_MOUSE	1	1	1	1	1
AC	P01631	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	IG KAPPA CHAIN V-II REGION 26-10.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE.				
RC	STRAIN=A/J;				
RX	MEDLINE=83178921; PubMed=6404298;				
RA	Novotny J., Margolies M.N.;				
RT	"Amino acid sequence of the light chain variable region from a mouse				
RL	anti-digoxin hybridoma antibody."				
CC	Biochemistry 22:1153-1158(1983).				
CC	-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA				
CC	PROTEIN THAT BINDS DIGOXIN.				
DR	PIR: A01914; KMS26.				
DR	InterPro: IPR003006; Ig_MHC.				
DR	InterPro: IPR003596; Ig_V.				
DR	Pfam: PF00047; Ig_V.				
DR	SMART: SM00406; IgV: 1.				
KW	Immunoglobulin V region; Monoclonal antibody; Hybridoma.				
FT	DOMAIN 1	23			
FT	DOMAIN 2	24			
FT	DOMAIN 3	39			
FT	DOMAIN 4	40			
FT	DOMAIN 5	54			
FT	DOMAIN 6	55			
FT	DOMAIN 7	61			
FT	DOMAIN 8	62			
FT	DOMAIN 9	93			
FT	DOMAIN 10	94			
FT	DOMAIN 11	102			
FT	DOMAIN 12	103			
FT	DISULFID	23			
FT	NON_TER	113			
SO	SEQUENCE	113 AA; 12273 MW; F9F39CE949A84C2A CRC64;			
Query Match	38.4%	Score 534; DB 1; Length 113;			
Best Local Similarity	92.0%	Pred. No. 7.6e-38;			
Matches	103;	Conservative 4; Mismatches 5; Indels 0; Gaps 0;			
QY	148	DVMTPTNPLSPVSLGDAASISCSRSSOSLHNSNTYLLHWLTKPPQSPPLTYKYSNRF 207			
DB	1	DVMTPTNPLSPVSLGDAASISCSRSSOSLHNSNTYLLHWLTKPPQSPPLTYKYSNRF 60			
QY	208	SGVPRFSGSGSGTDFTKISREAEADLGYFCSQSTHVPYTFGGGTKLEIK 259			
DB	61	SGVPRFSGSGSGTDFTKISREAEADLGYFCSQSTHVPYTFGGGTKLEIK 112			
RESULT	2				
KV2F_HUMAN					
ID	KV2F_HUMAN	STANDARD;	PRT;	133 AA.	

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AC P06310;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION RPMI 6410 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=6041852; PubMed=2997711;
RA Klobbeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT III."
RL Nucleic Acids Res. 13:6499-6513(1985).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sdb.ch).
CC -----
DR EMBL; 200020; CAA77315.1; -
DR PIR; A01890; K2HURP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 1 133 IG KAPPA CHAIN V-II REGION RPMI 6410.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 60 74 FRAMEWORK 2.
FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 82 113 FRAMEWORK 3.
FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 123 132 FRAMEWORK 4.
FT DISULFID 43 113 BY SIMILARITY.
FT NON TER 133
SQ SEQUENCE 133 AA; 14707 MW; 513C6A3673009EE CRC64;

Query Match 33.1%; Score 460; DB 1; Length 133;
Best Local Similarity 77.9%; Pred. No. 1.3e-31;
Matches 88; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

QY 147 GDVWTPPLPLPSLGDQASISCRSSQSLHNSGITYLHWYQKQSGPKLLIKVSNR 206
DB 20 GDVWTPPLPLPSLGDQASISCRSSQSLHNSGITYLHWYQKQSGPKLLIKVSNR 79
QY 207 FSGVDFRSGSGSGTDFTLKISRVEADLVGYFCQSSTHVPYFGGKTLEIK 259
DB 80 DSGVDFRSGSGSGTDFTLKISRVEADLVGYFCQSSTHVPYFGGKTLEIK 132

RESULT 3
KV2D_HUMAN STANDARD; PRT; 113 AA.
ID KV2D_HUMAN STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION TEM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (BENCE-JONES PROTEIN TEM).

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RX MEDLINE=74148480; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
RT primary amyloidosis."
RL Biochemistry 12:3763-3780(1973).
RN [2]
RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEM).
RX MEDLINE=73166638; PubMed=4700495;
RA Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
RA Glenner G.G.;
RT "Structural identity of Bence Jones and amyloid fibril proteins in a
RT patient with plasma cell dyscrasia and amyloidosis."
RL J. Clin. Invest. 52:1276-1281(1973).
CC -1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE URINE OF A
CC PATIENT WITH PLASMA CELL DYSPLASIA AND AMYLOIDOSIS.
CC -1- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
CC PATIENT WITH PLASMA CELL DYSPLASIA AND AMYLOIDOSIS.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
DR PIR; A01888; K2HUTW.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig_V.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein; Amyloid.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 40 54 FRAMEWORK 2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 62 93 FRAMEWORK 3.
FT DOMAIN 94 102 FRAMEWORK 4.
FT DOMAIN 103 112 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 23 93 BY SIMILARITY.
FT NON TER 113
SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81E1843CA CRC64;

Query Match 32.9%; Score 457; DB 1; Length 113;
Best Local Similarity 76.8%; Pred. No. 1.9e-31;
Matches 86; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 148 DVWTPPLPLPSLGDQASISCRSSQSLHNSGITYLHWYQKQSGPKLLIKVSNR 207
DB 1 DVWTPPLPLPSLGDQASISCRSSQSLHNSGITYLHWYQKQSGPKLLIKVSNR 60
QY 208 SGVDFRSGSGSGTDFTLKISRVEADLVGYFCQSSTHVPYFGGKTLEIK 259
DB 61 SGVDFRSGSGSGTDFTLKISRVEADLVGYFCQSSTHVPYFGGKTLEIK 112

RESULT 4
KV2E_MOUSE STANDARD; PRT; 113 AA.
ID KV2E_MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION 17S29.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Hybridoma;
RX MEDLINE=85128968; PubMed=6441768;
RA Aebersold R., Herbst H., Grutler T., Chang J.Y., Braun D.G.;
RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57Bl/6
RT origin: monoclonal antibodies 17S29.1 and 22S25.1 specific for the
RT group A-streptococcal polysaccharide."
RL Hoppe-Seivler's Z. Physiol. Chem. 365:1375-1383(1984).
CC -1- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
DR PIR; A01912; KVMS17.

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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 40 54 FRAMEWORK 2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 62 93 FRAMEWORK 3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 103 112 FRAMEWORK 4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA: 12390 MW: 4E93797046F8DB33 CRC64;

Query Match 32.6%; Score 454; DB 1; Length 113;
Best Local Similarity 75.9%; Pred. No. 3.4e-31;
Matches 85; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 148 DVVMTNPPLSLPVSLDDASISCRSSOSLLHSNGITLHWYLOKPGSPKLLIKVSNRF 207
DB 1 DVMVQAVFNSPVLTGTSASISCRSSKSLHSNGITLYWYLOKPGSPQLLYKSNLA 60

QY 208 SGVPPDRFSGSGSGTDFTLKISRVEAEDLGYVFCGSQSTHPVYFGGSKLEIK 259
DB 61 SGVPPDRFSGSGSGTDFTLRISRAEDGVGYVCAHNELEPYTFGGSKLEIK 112

RESULT 5
KVZE_HUMAN STANDARD; PRT; 117 AA.
ID KVZE_HUMAN
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION GM607 PRECURSOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobbeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
RT diversity."
RL Nature 309:73-76(1984).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: Z00009; -; NOT_ANNOTATED_CDS.
DR PIR: A01889; K2HUGH.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 1
FT NON_TER 1 1
FT CHAIN <1 4
FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
FT DOMAIN 5 27 FRAMEWORK 1.
FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 44 58 FRAMEWORK 2.
FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 66 97 FRAMEWORK 3.

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FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 107 116 FRAMEWORK 4.
FT DISULFID 27 97 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 12664 MW: 92C57DC719E559B1 CRC64;

Query Match 32.6%; Score 454; DB 1; Length 117;
Best Local Similarity 77.5%; Pred. No. 3.5e-31;
Matches 88; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 147 GDVMTNPPLSLPVSLDDASISCRSSOSLLHSNGITLHWYLOKPGSPKLLIKVSNR 206
DB 4 GDVMTQSPSLPVPYTPGPAISCRSSOSLLHSNGITLYWYLOKPGSPQLLYKSNR 63

QY 207 FSGVPPDRFSGSGSGTDFTLKISRVEAEDLGYVFCGSQSTHPVYFGGSKLEIK 259
DB 64 ASGVPPDRFSGSGSGTDFTLKISRVEAEDGVGYVCAHNELEPYTFGGSKLEIK 116

RESULT 6
KVZE_MOUSE STANDARD; PRT; 139 AA.
ID KVZE_MOUSE
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Botwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region."
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THE B1-8 MC CHAIN mRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: J00529; AAA38170.1; -.
DR PIR: A02034; MMS18.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV_1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA: 15419 MW: 1B57DD4FD0C9F465 CRC64;

```


RL Naturwissenschaften 56:195-205(1969).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.
DR PIR: A01885; K2HUCM.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
KM Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 24 95
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9E90A379569EC CRC64;

Query Match
Best Local Similarity 31.0%; Score 431.5; DB 1; Length 115;
Matches 85; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 148 DVWTPNPPLPVLPGDQASISCRSSQSLHS-NGITYLHWYLQKPGQSPKLLIKYSNR 206
Db 2 DIVWTPNPPLPVLPGEPASISCRSSQSLSDSGDNTYLNWYLQKAGQSPOLLITLSYR 61
QY 207 FSGVPCRFSSGSGCTDPTLKISRVEADLVYFCSSQSTHVPYFGGKLEIK 259
Db 62 ASGVPCRFSSGSGCTDPTLKISRVAEDVYVYCMQRLDIPYFGGKLEIR 114

RESULT 10
HV41_MOUSE STANDARD; PRT; 137 AA.
ID HV41_MOUSE
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=81234548; PubMed=6788376;
RA Boctwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
(NPB ANTIBODIES).
CC -----
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CC -----
CC EMBL: J00539; AAA38172.1; -.
DR PIR: A02038; GZMS43.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
IG HEAVY CHAIN V REGION S43.
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
FRAMEWORK 3.

FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF448BEC9 CRC64;

Query Match
Best Local Similarity 31.0%; Score 431.5; DB 1; Length 137;
Matches 86; Conservative 15; Mismatches 28; Indels 7; Gaps 2;

QY 3 SAIVLYVLLAAAHSAFAVVOLOQSGAEIVRGASVTLSCRASGYTFDYELHWVROTPV 62
Db 4 SCTMLF--LDAATRGVHSOVQLOQPEAEVYKPGASVYKLSCRASGTFSTYLMHWVNRPG 61
QY 63 HGLEWIGALDPETGTATYVQKFKRAIVTVDKSSSTAYMELRSLTSEDSAAVYYT----- 117
Db 62 RGLEWIGRIDPNNGGTTYNHFRSKATLTIDKPSSTAYMQLSLTSEDSAAVYCARVRLG 121
QY 118 RFEEDMGQGLTVYSA 133
Db 122 RYFDYWGQGTTLTVSS 137

RESULT 11
HV48_MOUSE STANDARD; PRT; 138 AA.
ID HV48_MOUSE
AC P03960;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR: A02033; HVMST7.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138
FT DOMAIN 21 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 127
FT DOMAIN 128 138
FT DISULFID 41 115
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 7481574C6907B8E CRC64;

Query Match
Best Local Similarity 30.4%; Score 423; DB 1; Length 138;
Matches 87; Conservative 14; Mismatches 28; Indels 8; Gaps 2;

QY 3 SAIVLYVLLAAAHSAFAVVOLOQSGAEIVRGASVTLSCRASGYTFDYELHWVROTPV 62
Db 4 SYTLIF--LVATGADVHSOVQLOQPEAEVYKPGASVYKLSCRASGTFSTYLMHWVNRPG 61
QY 63 HGLEWIGALDPETGTATYVQKFKRAIVTVDKSSSTAYMELRSLTSEDSAAVYY-----Y 116

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Db      62  OGLEWIGELPNDGRSNVNEKRNKATLVKSSSTAYMOJLSLPEFAVYCARSDGY 121
      117  TRAFEDMGOGTLTVSA 133
      122  YCMFYWGGGTLTVFSA 138

RESULT 12
KVZF_MOUSE STANDARD: PRT; 113 AA.
ID P01630:
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION 7534.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody, containing an additional cysteine residue.
RT Application of the dimethylaminoazobenzene isothiocyanate technique
RT for the isolation of peptides."
RL Biochem. J. 211:173-180(1983).
CC -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR: A01913; KMS7S.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 40 54 FRAMEWORK 2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 62 93 FRAMEWORK 3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 103 112 FRAMEWORK 4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 30.2%; Score 420; DB 1; Length 113;
Best Local Similarity 71.4%; Pred. No. 2.3e-28;
Matches 80; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 148 DYVMTNPPLSLPVSGDQASISCRSSQSLHSNGITVLMWYLOKPGOSPKLLIYKVSNR 207
      1 DIVVTQTPSALVTPGSSVTSICRSSKSLHSNGNTLWTFQRFQCCQLTIYMSNLA 60

Db      208  SGVPDRFSGSGGTFTLKISRVEADLGVYFCOSGTHVPTFGGKLEIK 259
      61  SGVPDRFSGSGGTFTLKISRVEADLGVYFCOSGTHVPTFGGKLEIK 112

RESULT 13
KVZC_HUMAN STANDARD: PRT; 112 AA.
ID P01616:
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION MTL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

QY 148 DYVMTNPPLSLPVSGDQASISCRSSQSLHSNGITVLMWYLOKPGOSPKLLIYKVSNR 207
      1 DIVVTQTPSALVTPGSSVTSICRSSKSLHSNGNTLWTFQRFQCCQLTIYMSNLA 60

Db      208  SGVPDRFSGSGGTFTLKISRVEADLGVYFCOSGTHVPTFGGKLEIK 259
      61  SGVPDRFSGSGGTFTLKISRVEADLGVYFCOSGTHVPTFGGKLEIK 112

RESULT 14
KVZC_MOUSE STANDARD: PRT; 117 AA.
ID HVI2_MOUSE
AC P01756:
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sidley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains."
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR: A02039; MMS4E.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
KW Immunoglobulin V region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .).
FT NON_TER 117 117
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Query Match 30.0%; Score 417.5; DB 1; Length 112;
Best Local Similarity 68.8%; Pred. No. 3.6e-28;
Matches 77; Conservative 19; Mismatches 15; Indels 1; Gaps 1;

QY 148 DYVMTNPPLSLPVSGDQASISCRSSQSLHSNGITVLMWYLOKPGOSPKLLIYKVSNR 207
      1 DIVVTQTPSALVTPGSSVTSICRSSQSLHSNGNTLWTFQRFQCCQLTIYMSNLA 60

Db      208  SGVPDRFSGSGGTFTLKISRVEADLGVYFCOSGTHVPTFGGKLEIK 259
      60  SGVPDRFSGSGGTFTLKISRVEADLGVYFCOSGTHVPTFGGKLEIK 111

RESULT 15
KVZC_MOUSE STANDARD: PRT; 117 AA.
ID HVI2_MOUSE
AC P01756:
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sidley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains."
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR: A02039; MMS4E.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
KW Immunoglobulin V region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .).
FT NON_TER 117 117
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

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OM protein - protein search, using sw model

Run on: January 18, 2002, 01:23:53 ; Search time 63.13 Seconds
(Without alignments)

623,274 Million cell updates/sec

Title: US-09-358-321C-32

Perfect score: 1391

Sequence: 1 MWSAIVLYVLLAAAHSAFA.....FGGTRKLEIKESKLISEEDL 269

Scoring table:

BLOSUM62

Gapop 10.0, Capext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_17:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_orfanelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rident:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	602.5	43.3	298	11 Q9QYF0	Q9QYF0 mus musculu
2	530	38.1	238	11 Q9QYF0	Q9QYF0 mus musculu
3	527	37.9	104	11 Q9JL82	Q9JL82 mus musculu
4	438	31.5	473	11 Q9D814	Q9D814 mus musculu
5	437.5	31.5	114	4 Q9UL80	Q9UL80 mus sapien
6	414	29.8	117	11 Q9QXFO	Q9QXFO mus musculu
7	409.5	29.4	463	11 Q9JL84	Q9JL84 mus musculu
8	407	29.3	473	11 Q9JL85	Q9JL85 mus musculu
9	405	29.1	117	11 Q9QXFO	Q9QXFO mus musculu
10	397	28.5	119	11 Q9JL86	Q9JL86 mus musculu
11	397	28.5	119	5 Q9GY22	Q9GY22 schistosoma
12	386.5	27.8	468	11 Q9JL81	Q9JL81 mus musculu
13	379.5	27.3	118	11 Q9JL84	Q9JL84 mus musculu
14	376.5	27.1	109	11 Q9JL85	Q9JL85 mus musculu
15	371.5	26.7	114	11 Q9JL81	Q9JL81 mus musculu
16	366	26.3	119	4 Q9UL94	Q9UL94 mus sapien
17	360.5	25.9	124	4 Q9UL92	Q9UL92 mus sapien
18	351.5	25.3	110	11 Q9JL77	Q9JL77 mus musculu
19	349	25.1	109	4 Q9UL78	Q9UL78 mus sapien

20	347	24.9	125	4 Q9UL95	Q9UL95 mus sapien
21	346	24.9	150	4 Q9Y298	Q9Y298 mus sapien
22	343.5	24.7	500	4 Q9BRV0	Q9BRV0 mus sapien
23	341	24.5	484	11 Q9JL86	Q9JL86 mus musculu
24	336.5	24.2	103	11 Q9JL80	Q9JL80 mus musculu
25	335.5	24.1	107	11 Q9ER29	Q9ER29 mus musculu
26	334.5	24.0	99	11 Q9JL74	Q9JL74 mus musculu
27	334.5	24.0	110	11 Q9JL83	Q9JL83 mus musculu
28	332	23.9	109	11 Q9JL85	Q9JL85 mus musculu
29	330	23.7	111	11 Q9D9B8	Q9D9B8 mus sapien
30	327.5	23.5	116	4 Q9UL89	Q9UL89 mus sapien
31	326.5	23.5	108	4 Q9UL77	Q9UL77 mus sapien
32	319	22.9	109	4 Q9UL86	Q9UL86 mus sapien
33	316.5	22.8	108	4 Q9UL83	Q9UL83 mus sapien
34	315.5	22.7	108	4 Q9UL70	Q9UL70 mus sapien
35	315	22.6	107	4 Q9UL81	Q9UL81 mus sapien
36	314.5	22.6	108	4 Q9UL79	Q9UL79 mus sapien
37	313	22.5	106	5 Q9UL10	Q9UL10 schistosoma
38	312	22.4	109	4 Q9UL85	Q9UL85 mus sapien
39	311.5	22.4	214	11 Q9JL85	Q9JL85 mus musculu
40	307.5	22.1	157	4 Q95978	Q95978 mus sapien
41	306.5	22.0	101	11 Q9UL78	Q9UL78 mus musculu
42	299.5	21.5	97	11 Q9UL76	Q9UL76 mus musculu
43	292	21.0	479	11 Q99M22	Q99M22 mus musculu
44	285	20.5	487	11 Q99KA4	Q99KA4 mus musculu
45	284.5	20.5	120	4 Q9B0A1	Q9B0A1 mus sapien

ALIGNMENTS

RESULT 1
ID Q9QYF0 PRELIMINARY: PRT: 298 AA.
AC Q9QYF0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CN 8 SCFV.
GN CN 8
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=SPLEEN;
RA Shinohara N., Demura T., Fukuda H.;
RL Submitted (Dec-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=SPLEEN;
RA Shinohara N., Demura T., Fukuda H.;
RL Submitted (Dec-1999) to the EMBL/GenBank/DBJ databases.
RT antibody recognizing a cell polarity using a phage-display subtraction method.
RT "Isolation of a novel type of vascular cell wall-specific monoclonal antibody recognizing a cell polarity using a phage-display subtraction method."
RT Submitted (Dec-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
DR EMBL: AB036341; BAA88633.1;
DR HSSP: P01607; IRET.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003586; IG_V.
DR Pfam: PF00047; 19; 2.
DR SMART: SM00406; 16v; 2.
SQ SEQUENCE 298 AA: 31867 MW; EDP96B8A17004317 CRC64;

Query Match 43.3%; Score 602.5; DB 11; Length 298;
Best Local Similarity 48.4%; Pred No. 5.7e+45;
Matches 122; Conservative 39; Mismatches 80; Indels 11; Gaps 4;
QY 14 AASAPAAVVOLOOGSALVPGASVTLSCKASGYTFDYELHWRQTFVHGLEWIGAIDP 73

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Db 33 AAOAPMAOVKLOQSGGGIVKPGCSLKLSCAASGDSFERYMWSVPOAPGKLEWISINP 92
OY 74 ETGGANVQKFKDAIYVDSSTAMELRSITSESAVY-----YTRWFEDMCGGL 128
Db 93 DSSITNTPSLKDKFTISRDNKNTLYLQMSKYRSEDTALTYCARASYGHSAYWGQGT 152
OY 129 VTSVAEGKSGSGSESKPG-DVWMPNPLSPVSLGQASISCRSSOSLHNSGITYLHW 187
Db 153 VTSVSGSGSGSGGGGSDIELTQSPASISASVGETVITTCRASGN-IHN----YLA 207
OY 168 YLQKRGSPKLLIKVNSRFGVPDRFSGSGSDTFTLKISRVEADLGVYFCGSOSTHP 247
Db 208 YQKRGKSPOLLVYNAKTADGVPSRFGSGSGTQYSLKINSIQPEDFGSYCOHFWTTP 267
OY 248 YTFGGGTGLEIK 259
Db 268 YTFGGGTGLEIK 279

RESULT 2
O99M37 PRELIMINARY; PRT; 238 AA.
AC 099M37;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
OS UNKNOWN (PROTEIN FOR MGC:5947).
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR;
RL Strussberg R.;
DR EMBL: BC002035; AA02035.1;
SQ SEQUENCE 238 AA; 26344 MW; PB2B06A0B801330A CRC64;

Query Match 38.1%; Score 530; DB 11; Length 238;
Best Local Similarity 90.2%; Pred. No. 9.7e-39;
Matches 101; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 148 DVWMPNPLSPVSLGQASISCRSSOSLHNSGITYLHWLQKRGSPKLLIKVNSNR 207
Db 20 DVWMPNPLSPVSLGQASISCRSSOSLHNSGITYLHWLQKRGSPKLLIKVNSNR 79
OY 208 SGVPDRFSGSGSDTFTLKISRVEADLGVYFCGSOSTHPYTFGGGTGLEIK 259
Db 80 SGVPDRFSGSGSDTFTLKISRVEADLGVYFCGSOSTHPYTFGGGTGLEIK 131

RESULT 3
O9ULB2 PRELIMINARY; PRT; 104 AA.
AC 09ULB2;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C;
RA Maikael S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

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CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF206024; AAF69322.1;
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IG; 1.
FT NON_TER 1
FT TER 1
FT NON_TER 104
FT TER 104
SQ SEQUENCE 104 AA; 11360 MW; 5DABBFDF5F0A1AE CRC64;

Query Match 37.9%; Score 527; DB 11; Length 104;
Best Local Similarity 96.2%; Pred. No. 5.9e-39;
Matches 100; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 156 LSLPVSLGQASISCRSSOSLHNSGITYLHWLQKRGSPKLLIKVNSRFGVPDRFS 215
Db 1 LSLPVSLGQASISCRSSOSLHNSGITYLHWLQKRGSPKLLIKVNSRFGVPDRFS 60
OY 216 GSGSGTDTFTLKISRVEADLGVYFCGSOSTHPYTFGGGTGLEIK 259
Db 61 GSGSGTDTFTLKISRVEADLGVYFCGSOSTHPYTFGGGTGLEIK 104

RESULT 4
O9DBL4 PRELIMINARY; PRT; 473 AA.
AC 09DBL4;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE 1810060009RIK PROTEIN.
GN 1810060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shimagawa A., Shibata K., Yoshino M., Ishii Y.,
RA Akizawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirini L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustingich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzerelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seye T., Shibata K., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whittaker C., Wilming L.,
RA Wyszewski A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 408:685-690(2001).
-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AK007918; BAB25349.1;
DR MGD: MGI:1924014; 1810060009RIK.
DR InterPro: IPR003599; IG.
DR InterPro: IPR003597; IG_C1.
DR InterPro: IPR003600; IG_Like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG; 4.
DR SMART: SM00409; IG; 2.

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DR SMART: SM00407; IG1, 3.
 DR SMART: SM00406; IGV, 1.
 DR SMART: SM00410; IG_1like, 1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 SO SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 31.5%; Score 438; DB 11; Length 473;

Best Local Similarity 52.5%; Pred. No. 2.9e-30;
 Matches 95; Conservative 21; Mismatches 45; Indels 20; Gaps 3;

QY 7 LYLVLAAAHSAFAVLOOGSGAELVRPGASVTLSCKASGYFTDYELHWRQTPVHGLE 66
 DB 6 VFELFLSVTAGVHCQYOLQSGAELVRPGASVTKISKASGYFTDYELHWRQTPVHGLE 65
 QY 67 WIGALIDPETGCTAYNCRFKDAIVYDKSSSTAYMELRLTSEDSAVYYTR-----WF 120
 DB 66 WICKIGPGSGSYNEKFKGKATLTADKSSSTAYWQLSLTSEDSAVYECARSGYDWMF 125
 QY 121 EDMGCGTLVYSAEGKSSSS-----GSESKGDVY--MTNPPLSLPVSLGDQA 166
 DB 126 AYWCGGLVTVSAKTTAPSVYPLAPVCGGTGSSVTLGCLVKGYPPEPVLTLWNSGLS 185
 QY 167 S 167
 DB 186 S 186

RESULT 5

Q90L80 PRELIMINARY; PRT; 114 AA.

ID Q90L80;
 AC Q90L80;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL: AF035034; AAD56270.1; -.
 DR InterPro: IPR003006; I9_MHC.
 DR InterPro: IPR003596; I9_V.
 DR Pfam: PF00047; I9_1.
 DR SMART: SM00406; IGV, 1.
 FT NON_TER 1
 FT NON_TER 114
 SO SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 31.5%; Score 437.5; DB 4; Length 114;

Best Local Similarity 76.1%; Pred. No. 4.7e-31;
 Matches 66; Conservative 13; Mismatches 13; Indels 1; Gaps 1;

QY 148 DVMTPNPPLSLPVSLGDQASISCRSSQSLHNSNGITLHWYLOKPGQSKFLIYKVSNR 207
 DB 1 DVMATGSLPLVTLRQPAISICRSSQSPVSDGNTYLNWFOQRPGQSPRRILYKVSNRD 60
 QY 208 SGVADPRSGSGTDFTLKISRVEADLGVYFCSTH-VPTFGGGRKLEIK 259
 DB 61 SGVADPRSGSGTDFTLKISRVEADLGVYFCSTH-VPTFGGGRKLEIK 113

RESULT 6
 ID Q90XFO PRELIMINARY; PRT; 117 AA.
 AC Q90XFO;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Clemens A., Rademakers A., Specht C., Koelsch E.;
 RA Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL: AJ225171; CAB65236.1; -.
 DR InterPro: IPR003006; I9_MHC.
 DR InterPro: IPR003596; I9_V.
 DR Pfam: PF00047; I9_1.
 DR SMART: SM00406; IGV, 1.
 FT NON_TER 1
 FT NON_TER 117
 SO SEQUENCE 117 AA; 13060 MW; D816AD0858A47EAC CRC64;

Query Match 29.8%; Score 414; DB 11; Length 117;
 Best Local Similarity 69.8%; Pred. No. 5.7e-29;
 Matches 81; Conservative 13; Mismatches 18; Indels 4; Gaps 1;

QY 22 VOLOQSGALVRPGASVTLSCKASGYFTDYELHWRQTPVHGLEWIGALIDPETGCTAYN 81
 DB 2 VOLOQSGALVRPGASVTKISKASGYFTDYELHWRQTPVHGLEWIGALIDPETGCTAYN 61
 QY 82 QKFKKATLTVDKSSSTAYMELRLTSEDSAVYYTR-----WFDWGGGTLVYSA 133
 DB 62 QKFKKATLTVDKSSSTAYMELRLTSEDSAVYYCARQKDYFDWGGGTLVYSS 117

RESULT 7

Q99LC4 PRELIMINARY; PRT; 463 AA.

ID Q99LC4;
 AC Q99LC4;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE SIMILAR TO RIKEN CDNA 161006009 GENE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC003435; AAH03435.1; -.
 SO SEQUENCE 463 AA; 51007 MW; EAA674C6BHC30783 CRC64;

Query Match 29.4%; Score 409.5; DB 11; Length 463;
 Best Local Similarity 50.8%; Pred. No. 8.9e-28;
 Matches 94; Conservative 16; Mismatches 50; Indels 25; Gaps 4;

QY 5 IYLYVL-AAAASAFAAVLOOGSGAELVRPGASVTLSCKASGYFTDYELHWRQTPVH 63
 DB 6 IYLYVL-AAAASAFAAVLOOGSGAELVRPGASVTLSCKASGYFTDYELHWRQTPVH 62
 QY 64 GLEWIGALIDPETGCTAYNCRFKDAIVYDKSSSTAYMELRLTSEDSAVYYTR----- 118
 DB 63 GLEWIGALIDPETGCTAYNCRFKDAIVYDKSSSTAYMELRLTSEDSAVYCARSSYS 122

QY 119 --WEDWGGGLVTVASABGKSSGSGESKPGDVVWT-----PNPLSLPVSL 162
 Db 123 YDLFAWGGGLVTVASAKTTPPSVYPLAPGSAQTNMVLGLGVKGYFPEPVTVWNS 182
 QY 163 GDQAS 167
 Db 183 GSLS 187

RESULT 8
 099L25 PRELIMINARY: PRT: 473 AA.
 AC 099L25:
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE SIMILAR TO RIKEN CDNA 181006009 GENE.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC003888; AA03888.1; -
 SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 29.3%; Score 407; DB 11; Length 473;
 Best Local Similarity 48.1%; Pred. No. 1.5e-27;
 Matches 90; Conservative 24; Mismatches 45; Indels 28; Gaps 4;
 QY 6 YLYVLLAAASAFANVQLQSGALVPRGASVYLSKASGYTFTDYEIHVROTYPVHGL 65
 Db 8 LFFLSVTVGHS--QVQSQSDAELVPRGASVYKISCVSGYFTDHTIHVWKQRPQGL 64
 QY 66 EWIGADIPETGATVNOCKKCAITVVDKSSSTAYMELRSLTSDSAVYYTR----- 118
 Db 65 EWGVIYPRDGTSTKNEKKGATLTADKSSSTAYMQLNLTSDSAVCFSGSGSIYXG 124
 QY 119 ---WEDWGGGLVTVASABGKSSGSGESKPGDVV--MTPNPLSLPV 160
 Db 125 YGLYVLDYWGQGLTITVSAKTTAPSVYPLAPVCGDTTGSVTVGLGVKGYFPEPVTLTW 184
 QY 161 SLDQAS 167
 Db 185 NSGSLSS 191

RESULT 9
 090XE9 PRELIMINARY: PRT: 117 AA.
 AC 090XE9:
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Clemens A., Rademakers A., Specht C., Koelsch E.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL: AJ225174; CAB65237.1; -
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IGV; 1.

FT NON-TER 1
 FT NON-TER 117
 SQ SEQUENCE 117 AA; 13000 MW; CDDZAF84D499734 CRC64;

Query Match 29.1%; Score 405; DB 11; Length 117;
 Best Local Similarity 69.8%; Pred. No. 3.5e-28;
 Matches 81; Conservative 11; Mismatches 20; Indels 4; Gaps 1;
 QY 22 VOLQSGALVPRGASVYLSKASGYTFTDYEIHVROTYPVHGLWIGALDIPETGATVYN 81
 Db 2 VOLQSGELVPRGASVYMSCKASGYTFTDYIMKMWQSHGSKLEWIGDINPNNGTSYN 61
 QY 82 QKFKAATVYDKSSSTAYMELRSLTSDSAVYYTR---WEDWGGGLVTVSA 133
 Db 62 QKFKAATLVDRKSSSTAYMQLNLTSDSAVYVCARDRYAMDYWGQTSYVSS 117

RESULT 10
 092IC6 PRELIMINARY: PRT: 117 AA.
 AC 092IC6:
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE ANTI-PORCINE VCAW MAB 2A2 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C.
 RA Mueller J.P., Gianconi M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
 RA Matis L.M., Evans M.J.;
 RT "Humanized porcine VCAW-specific monoclonal antibodies with chimeric
 RT IgG2/G4 constant regions block human leukocyte binding to porcine
 RT endothelial cells";
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL: D78799; AAD00291.1; -
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IGV; 1.
 FT NON-TER 1
 FT NON-TER 117
 SQ SEQUENCE 117 AA; 13122 MW; 4F65B193AFB77E5B CRC64;

Query Match 28.5%; Score 397; DB 11; Length 117;
 Best Local Similarity 67.2%; Pred. No. 1.8e-27;
 Matches 78; Conservative 9; Mismatches 25; Indels 4; Gaps 1;
 QY 22 VOLQSGALVPRGASVYLSKASGYTFTDYEIHVROTYPVHGLWIGALDIPETGATVYN 81
 Db 2 VOLQSGPOLVPRGASVYKISCVSGYFTDHTIHVWKQRPQGL 64
 QY 82 QKFKAATVYDKSSSTAYMELRSLTSDSAVYYTR---WEDWGGGLVTVSA 133
 Db 62 QRLKDAITLVKSSSTAYMQLNLTSDSAVYCTREVSWMFVWGGGLVTVSA 117
 RESULT 11
 09GYZ2 PRELIMINARY: PRT: 119 AA.
 AC 09GYZ2:
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE MONOCLONAL ANTI-ID10TYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
 DE (FRAGMENT).

OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
 OC Trematoda; Digenea; Strigeidae; Schistosomatidae; Schistosomatidae;
 OC Schistosoma.
 OX NCBI_TaxID=6182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Song X.T., Feng Z.Q., Guan X.H.;
 RT "Amplification, cloning and sequence analysis of the heavy chain
 RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
 RT Schistosoma japonicum."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC EMBL: AF282622; AAC01452.1; -
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00409; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 DR SMART: SM00410; IG_Like; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;

Query Match 28.5%; Score 397; DB 5; Length 119;
 Best Local Similarity 65.3%; Pred. No. 1.8e-27;
 Matches: 77; Conservative 14; Mismatches 21; Indels 6; Gaps 1;

OY 22 VOLOSGAEIVRPGASVTLSCKASGYFTDYEIHWRQTPVHGLEWIGALIDPETGTAYN 81
 DB 2 VOLVESGAEVRKPGASVTLSCKASGYFTDYEIMWVQAGHGLEWIGITNPSRGITNN 61
 OY 82 QKFKDKAIVTVDKSSSTAYMELSLTSEDSAVYYVYTFMPED-----WGQGLVTVSA 133
 DB 62 QKFKDRAVTVTKDSFTAYMDRLSLRSADSAVYYCAHYDHCCLDYWGQGLTVTVSS 119

RESULT 12
 O99LJ31 PRELIMINARY; PRT; 468 AA.
 ID O99LJ31.
 AC O99LJ31.
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC003878; AAH03878.1; -
 SQ SEQUENCE 468 AA; 51661 MW; 963523283332ADB CRC64;

Query Match 27.8%; Score 386.5; DB 11; Length 468;
 Best Local Similarity 47.3%; Pred. No. 9.4e-26;
 Matches 86; Conservative 26; Mismatches 49; Indels 21; Gaps 4;
 OY 6 VLYVLAASAFAAVALOOSGAELVRPGASVTLSCKASGYFTDYEIHWRQTPVHGL 65
 DB 6 VIFELMAVVI-GVNSEVQLQOSGAELVRPGASVTLSCAGFNKXDSLMHWQRPREGGI 64
 OY 66 EWIGALIDPETGTAYNOKFKKAIIVTVDKSSSTAYMELSLTSEDSAVYI-----YTRM 119
 DB 65 EWIGIDPEDETKYAPKFDKATITADTSSNTAYLQSLSLTSBDAIYYCARNLLYGGY 124

OY 120 FEDMGQGLTVTSAEKKSSGS-----GSESKPGDV--MTPNLSLVSLDQ 165
 DB 125 YDWGQGLTVTVSSAKTAPSYPLAPVCGDTGSSSVTLGCLVKGFEPYVTLWNSSGL 184
 OY 166 AS 167
 DB 185 SS 186

RESULT 13
 O921C4 PRELIMINARY; PRT; 118 AA.
 ID O921C4.
 AC O921C4.
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA1B/C;
 RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
 RA Mattis L.M., Evans M.J.;
 RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
 RT 1962/64 constant regions block human leukocyte binding to porcine
 RT endothelial cells."
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC EMBL: U78801; AAD00293.1; -
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 118 AA; 13036 MW; 90EC559D31EC4FC CRC64;

Query Match 27.3%; Score 379.5; DB 11; Length 118;
 Best Local Similarity 65.0%; Pred. No. 6.1e-26;
 Matches 76; Conservative 11; Mismatches 25; Indels 5; Gaps 1;

OY 22 VOLOSGAEIVRPGASVTLSCKASGYFTDYEIHWRQTPVHGLEWIGALIDPETGTAYN 81
 DB 2 VOVOOSGAELARPASVTLSCKASGYFTDYEIMWVQAGHGLEWIGITNPSRGITNN 61
 OY 82 QKFKDKAIVTVDKSSSTAYMELSLTSEDSAVYYVYTR---WFEDMGQGLTVTVSA 133
 DB 62 QKFKRAVTVTKDSFTAYMDRLSLRSADSAVYYCARNRYGDFYWGQGLTVTVSS 118

RESULT 14
 O92L75 PRELIMINARY; PRT; 109 AA.
 ID O92L75.
 AC O92L75.
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA1B/C;
 RA Maiktel S., Liao L., Cunningham M.W., Diamond B.;
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
 RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC EMBL: AF206031; AAF69329.1; -
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IGv; 1.
 FT NON_TER 1
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 12118 MW; FF65B41BBF936A6 CRC64;

Query Match 27.1%; Score 376.5; DB 11; Length 109;
 Best Local Similarity 67.9%; Pred. No. 1e-25;
 Matches 74; Conservative 10; Mismatches 20; Indels 5; Gaps 1;

QY 30 ELVPRGASVTLSCKASGYFTDYEIHWRQTPVHGLEWIGAIDPETGGTAVNCKRKDKAI 89
 DB 1 ELVPRGASVTLSCKASGYFTSYVHWYKQKPGQGLEWIGYINPYNDGTRKNEKFKGKAT 60
 QY 90 VTVDKSSSTAYMELRSLTSEDSAVYYT---RWFEEDWGQGLTVTSA 133
 DB 61 LTSDKSSSTAYMELSLTSEDSAVYYCCARDGNYRGFDYWGQGLTVTSS 109

RESULT 15
 09JL81
 ID 09JL81 PRELIMINARY; PRT; 114 AA.
 AC 09JL81;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
 DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RA Malxiei S.; Liao L.; Cunningham M.W.; Diamond B.;
 RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
 acetyl-glucoamine antibodies from mice with autoimmune myocarditis."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN
 CC EMBL: AF206025; AAF69323.1; -
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_V.
 DR Pfam: PF00047; IG_1.
 DR SMART: SM00406; IGv; 1.
 FT NON_TER 1
 FT NON_TER 114
 SQ SEQUENCE 114 AA; 12829 MW; 404855FDE6BA56F8 CRC64;

Query Match 26.7%; Score 371.5; DB 11; Length 114;
 Best Local Similarity 64.6%; Pred. No. 2.9e-25;
 Matches 73; Conservative 11; Mismatches 20; Indels 9; Gaps 1;

QY 30 ELVPRGASVTLSCKASGYFTDYEIHWRQTPVHGLEWIGAIDPETGGTAVNCKRKDKAI 89
 DB 2 QLVPRGASVTLSCKASGYFTSYVHWYKQKPGQGLEWIGIDPSDSETRLNCKRKDKAT 61
 QY 90 VTVDKSSSTAYMELRSLTSEDSAVYYT---RWFEEDWGQGLTVTSA 133
 DB 62 LTVDKSSSTAYMQLSPTSEDSAVYYCCARSNYGSSLYYFDYWGQGLTVTSS 114

Search completed: January 18, 2002, 01:31:24
 Job time: 451 sec

